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Aag80107 Human CCR
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Adf56627 Partial h Adm67224 Murine ad Adc92922 Mouse GPC Adc99228 Mourine CPC Add74040 Murine CC Add44869 Amino aci Aaw57037 Mouse CC Add44869 Rat Prote Add44869 Rat Prote Add44863 Rat Prote Aaw27123 Human CCR Aaw27123 Human CCR Aaw27123 Human CCR Aaw27123 Human CCR Aaw27121 Human CCR Aaw88232 HIV-1 co- Aae07048 Human G-p Aag80111 Human CCR Aae07048 Human G-p Aae07039 Human G-p		receptor MCP-1RA. tor; MCR-1R; chemokine. '		
ADF56627 ADM67224 ADO29222 ADD29404 ADD79089 AAM79089 ADM44869 ADM44869 AAW27123 AAW27125 AAW	ALIGNMENTS 374 AA.) ctant protein-1 rec protein-1 receptor;	/Qualifiers extracellular transmembrane transmembrane transmembrane transmembrane	178 = transmembrane 231 266 = transmembrane 313 = transmembrane 315 = carboxyl tail
7.6.6 7.7.6 7.	standard; protein;	revised) Eirst entry Chemoattra Sttractant	Location/Qualifiers 148 /label= extracellul 4970 /label= transmembra 80700 /label= transmembra 115136	154178
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	RESULT 1 AAR79165 ID AAR7 XX AC AAR7	8 X X X X X X X X X X X X X X X X X X X	XELLLLLL	X8XX222222X

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N-PSDB; AAQ96297.

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DNA encoding monocyte chemo-attractant protein-1 receptor - used partic.
For identifying antagonists and for treating diseases characterised by
T monocytic infiltrates.

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Claim 2; Fig 1; 84pp; English.

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Claim 2; Fig 1; 84pp; English.

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Claim 2 is regeler to the conserved

Gegenerate oligo primers were designed corresp. to the conserved

Gegenerate oligo primers were designed corresp. to the conserved

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Gegenerate oligo primers were designed corresp. The degenerate

CC domains of the MIP-labla/ARAWTES receptor, the IL-8 receptors and the

HUNGTRS orphan receptor (GenBank Accession #M99293. The degenerate oligo

CC OGS300. Amplification of CDNA derived from MM6 cells with the primers

CC OGS300. Amplification of CDNA derived from MM6 cells with the primers

CC OGS300. Amplification of CDNA derived from MM6 close a novel

protein. To obtain a full-length version of this close, a MM6 cDNA

CC DEAD COMPA close was obtd. Analysis of additional closes in the MM6 cDNA

CC Aransmembrane domain but contained a different cytoplasmic tail. The CR

CC Transmembrane domain but contained a different cytoplasmic tail. The second sequence appears to represent alternative splicing of the carboxyl

CC transmembrane domain but contained a different cytoplasmic tail. The manner of the MCP-IRB (see Q6297/R79165 & Q6298R79166). Active mature MCP-

CC LETMinal tail of the MCP-IR protein. The two sequences are denoted MCP-

CR has a predicted mol. wt. of about 42,000 daltons. MCP-IRB has a mol.

CC MC about 41,000 daltons. (Updated on 25-MAR-2003 to correct PN

CC Eield.)

SQ Sequence 374 AA;
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Sequence 374 AA;
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AAG80107 standard; protein; 374 AA.

RESULT 2

(first entry)

17-JAN-2002

AAG80107;

AAGB0107 ID AAGB XX XX AAC AAGB XX IT-J XX IT-J XX DE Huma

Human CCR2a protein

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This invention describes a novel diagnostic agent (A) comprising at least two different ligands (I) for receptors (II) that are implicated in disease. (A) are used for the diagnosis of tumors (especially colorectal or prostatic), organ rejection, inflammation and autoimmune diseases. Also inhibitors of (I) are used therapeutically against tumors (and their metastases), inflammation (particularly bronchial asthma or chronic bowel inflammation), or autoimmune diseases (rheumatoid arthritis or lupus), where the (cardio) vascular, lymphatic, respiratory, nervous, digestive, endocrine, motor or urogenital systems or skin are affected, and bone marrow diseases. The products of the invention are chemokine derivatives which have cytostatic, antifilammatory, antiasthmatic, immunosuppressive, dermatological, antifhemmatory calls through a chemokines act on specific tumor and inflammatory calls through a constellation of chemokine (CR), which control migration and proliferation of these calls. Ad880148 represent human chemokine fragments used to illustrate the method of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Diagnostic agent containing two or more receptor-specific ligands, useful for detecting tumors, inflammation etc., also therapeutic use of ligand inhibitors.
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                                    inflammation, autoimmune disease; metastasis; bronchial asthma; lupus; chronic bowel inflammation; rheumatoid arthritis; cytostatic; antiinflammatory; antiasthmatic; immunosuppressive; dermatological;
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                   colorectal; prostatic; organ rejection;
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                 Chemokine; tumour diagnosis;
                                                                                                   antirheumatic; antiarthritic
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Best Local Similarity 100.
Matches 374; Conservative
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(FORS/) FORSSMANN U.
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Human; thymus expressed chemokine; TECK; chemokine; MIP-3alpha; receptor; MIP-3beta; dendritic cell receptor for chemokine; DC CR; M/DC CR; asthma; monocyte/dendritic cell receptor for chemokine; inflammatory condition; abnormal physiology; abnormal proliferation; degeneration; atrophy; antiasthmatic; cytostatic; chemokine receptor-2; CKR-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New chemokines, TECK, MIP-3 alpha, MIP-3 beta, DC CR and M/DCCR, useful for treating conditions associated with abnormal physiology or development, including inflammatory conditions (e.g. asthma), and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zlotnik A;
                                                                                                                                                                                                                                                                                  Human chemokine receptor-2 (CKR-2) polypeptide.
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                                                                                                                                                                               ABU09083 standard; protein; 374
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96US-0028329P.
97US-0048593P.
97US-00887977.
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                                                                   GRAPEASLQDKEGA 374
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121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
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                181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR
                                                                                                                                      181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR
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61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; pain; neuronal tissue; gene therapy;
spinal segmental nerve injury; chronic constriction injury; CCI;
spared nerve injury; SNI; Chung.
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN

Best Local Similarity 100. Matches 374; Conservative

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that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the control of the polypeptides given in the specification, a method for identifying a compound useful in treating to pain and a pharmaceutical composition comprising the one or more of pain and a pharmaceutical composition comprising the one or more condulates its activity is useful for preparing a medicament for treating condulates its activity is useful for preparing a medicament for treating conjugation (cit) and spared nerve injury (SNI) in an animal (e.g. gene injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene the specification) which is differentially expressed during pain. Note:

The sequence data for this patent did not form part of the printed contains an expectation of the printed contains an expectation of the printed contains an expectation of the printed contains and expectations are secured and any expressed during pain.
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100.0%; Score 1970; DB 7; Length 374; 100.0%; Pred. No. 5.1e-215; tive 0; Mismatches 0; Indels 0
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The invention discloses a composition comprising two or more isolated rat or human polymucleotides or a polymucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the nucleic acid sequence. Also claimed are a vector comprising the novel polymucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying a nucleotide sequence that increases or decreases the expression of the polymucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the composition, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more copelypeptides or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (CMUMB), in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note:

specification, but was obtained in electronic form directly from WIPO at

New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.

Claim 1; Page; 1017pp; English.

Costigan M;

Befort K,

Woolf C, D'urso D, WPI; 2003-268312/26. GENBANK; P41597.

14-AUG-2002; 2002WO-US025765. 14-AUG-2001; 2001US-0312147P. 26-NOV-2001; 2001US-033347P (GEHO) GEN HOSPITAL CORP. (FARB) BAYER AG.

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100.0%; Pred. No. 5.1e-215;
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Human; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

WO2003016475-A2 Homo sapiens

Human Protein P41597, SEQ ID NO 10296

29-JAN-2004 (first entry)

ADD44865;

ADD44865 standard; protein; 374 AA.

RESULT 5 ADD44865

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The invention relates to a novel method for diagnosing and analysing autoimmune disease or arthritides. The method comprises obtaining a sutoimmune disease or arthritides. The method comprises obtaining a patient sample containing mRNA, analysing gene expression using the mRNA that results in a gene expression signature of the mRNA, and using that gene expression signature to diagnose or analyse the autoimmune disease or arthritides in the patient, where gene expression of at least 60% of the genes correlates with that of the gene expression of at least 60% of the genes correlates with that of the gene expression of at least 60% of the genes correlates with that of the gene expression of arthritis; dentification of curther comprises: a treatment of rheumatoid arthritis in a mammal conter than a mouse; diagnosis of rheumatoid arthritis in a mammal, and array or gene chip, specific for rheumatoid arthritis in a mammal, and array or gene chip, specific for rheumatoid arthritis; screening the analyses of autoimmune disease or theumatoid arthritis; screening the induced arthritis; and reducing the symptoms associated with collagentinduced arthritis. The compositions of the invention have the following activities: immunosuppressive, antirheumatic, antiarthritides, such as antigout, antiinflammatory, dermatological, and immunosuphatory. The methods and compositions of the present invention are useful for diagnosing and treating autoimmune disease or arthritides, such as rheumatoid arthritis, lupus, ankylosing spondyllitis, fibrositis,
                                                                                                                          360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        autoimmune disease; arthritide; gene expression analysis; rheumatoid arthritis; collagen-induced; immunosuppressive; antirheumatic; antiarthritic; osteopathic; antigout; antiinflammatory; dermatological; immunomodulatory; lupus; ankylosing spondylitis; Fibrositis; fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Diagnosing and analyzing autoimmune disease using gene expression profiles and microarray technology, useful for diagnosing and treating rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and
                                                                                                                                                                                                        360
NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI
                                                                                                                                                                        301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human chemokine (C-C motif) receptor 2, isoform A, chemokine (C-C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADP65146 standard; protein; 374 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-OCT-2002; 2002WO-US035433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-OCT-2001; 2001US-0336220P
                                                                                                                                                                                                                                                                              361 GRAPEASLQDKEGA 374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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ADP66146

ADP661
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fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an immune disease caused by an infectious agent. This sequence represents a protein sequence relating to the genes used in the analysis and treatment of autoimmune diseases or arthritides. Note: This sequence is not shown in the specification. It has been supplied in an electronic format from
                                                                                                                                                                                                                                                                                                                                                             120
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                                                                                                                                                                                                                                                                                                                                                                                                                                             121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
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                                                                                                                                                                                                                                                                                                                                                                                       1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN
                                                                                                                                                                                                                                                                                                      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN
                                                                                                                                                                                                                                                                                                                                                             61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY
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                                                                                                                                                                                         Length 374;
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                                                                                                                                                                                         100.0%; Score 1970; DB 7; 100.0%; Pred. No. 5.1e-215;
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                                                                                                                                                                                                        100.0%; Pred. ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       361 GRAPEASLQDKEGA 374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-JUL-2004 (first entry)
                                                                                                                                                                                                                                     Matches 374; Conservative
                                                                                                                                                                                                                 Similarity
                                                                                                                                                    Sequence 374 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO20040400000-A2
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                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                   Best Local
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181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240
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                                                                                                                                                                                                                                                                                                                                                                                               ADQ67847 standard; protein; 374 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human chemokine receptor CCR-2.
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11-OCT-1996; 96US-0028129P.
04-JUN-1997; 97US-004853P.
03-JUL-1997; 97US-00887977.
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                                                                                                                                                                                                                                                                              361 GRAPEASLODKEGA 374
                                                                                                                                                                                                                                   GRAPEASLODKEGA 374
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GISH K C.
SCHALL T J.
VICARI A.
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(GISH/) C
(SCHA/) S
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(ZLOT/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to human and mouse G protein-coupled receptors (GPCRs) and nucleic acids encoding them. The invention also relates to sequences at least 90% identical to the GPCR proteins and nucleic acids of the inventing or diagnosing diseases associated with GPCRs of the inventing, preventing or diagnosing diseases associated with GPCRs of the invention; methods of screening for compounds useful in the treatment of GPCR-related diseases; a transgenic compounds useful in the treatment of GPCR-related diseases; a transgenic mouse comprising a GPCR transgene or in an endogenous GPCR gene; cells derived from the trasngenic mice; kits comprising several mice, each of which has a mutation in a different GPCR polymucleotides of the invention; and kits comprising comprising several mice, each of which has a mutation in a different GPCR polymucleotides of the invention. The city probes which hybridise to GPCR polymucleotides of the invention. The city probes which hybridise to GPCR polymucleotides of the invention. The disponsion is treatment or prevention of a wide variety of the unvention further discloses variants of the GPCR polympetides and vectors comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may be used in the diagnosis, treatment or prevention of a wide variety of diseases including neurological disorders (e.g., Alzheimer's disease, depression, diabetic neuropathy, Parkinson's disease or schizophrenia); disorders of the color or intestine disorders of compound or leukaemia); immune disorders (e.g., augina, cardiac arrhythmia or maemia or leukaemia); immune disorders (e.g., augina, cardiac arrhythmia or Alder and joint disorders (e.g., augina, bone disorders or Alder and disorders (e.g., augina, bone and joint disorders (e.g., augina, contributed deficiency-related diseases); and disorders of the kidmey, liver, lung, brostate, testis, skin, stomach, pancreas, spleen, thymus and character, testis, skin, stomach, pancreas, spleen, thymus and control or the printed specification; those
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                                                                                                                                                                                   JE, Gragerov A, Hohmann J, Li F;
Pavlova MN, Vassilatis D, Zeng H;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 151; SEQ ID NO 322; 542pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                 pectoris, Parkinson's disease.
                          09-SEP-2003; 2003WO-US028226
                                                                   09-SEP-2002; 2002US-0409303P
09-APR-2003; 2003US-0461329P
                                                                                                                                                                                   Gaitanaris GA, Bergmann
Madisen L, Mcilwain KL,
                                                                                                                                                                                                                                                         WPI; 2004-390329/36.
N-PSDB; ADO29829.
                                                                                                                                        (PRIM-) PRIMAL INC.
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The invention relates to a substantially pure or isolated polypeptide comprises the mature protein of human TECK (thymus expressed chemokine) whose full length sequence appears as ADGG7837. Also included are an isolated or recombinant nucleic acid, a host cell comprising the area in vector comprising the nucleic acid, a host cell comprising the expression wouse TECK cDNA and protein, thuman chemokines MIP-3alpha and MIP-3beta (and their encoding cDNAS), and the cDNAS and encoded proteins corresponding to human chemokine receptors DCCR (dendritic cell receptor for chemokine) and MDCCR (Monocyte/Gendritic cell receptor chemokine). The polypeptide is useful for treating conditions associated with abnormal physiology or development, including inflammatory conditions, e.g. asthma. The present sequence represents a human
                                                                                                                                                                                                                                                                                                        360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; receptor; thymus expressed chemokine; TECK; MIP-3alpha; MIP-3beta; chemokine receptor; DCCR; dendritic cell receptor for chemokine; M/DCCR; Monocyte/dendritic cell receptor for chemokine; abnormal physiology; development; inflammatory condition; asthma.
                                                                                                                                                                                                                                                        301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGRUVKVITQGLLDGRGKGKSI
241 AVRVIPTIMIVYFLFWTPYNIVILLINTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI
                                               241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI
                                                                                                                                                                                                        301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI
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(HUMA-) HUMAN GENOME SCI INC.
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                      Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 344 AA;
                      Roschke V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
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ABU61655
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                                                                                                                                          NPIIYAFVGEKFRSLFHIALGCRIAPLOXPVCGGPGYRPGKNVKVTTQGLLDGRGKGKSI 360
                                                                                                                                                                          121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
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                                                                                                                                                                                                                                                                                                           NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360
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                                                                                                 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunoglobulin, variable heavy chain, variable light chain, human, G-protein chemokine receptor; CCR5, HDGNR10; cancer; inflammation; immunologic deficiency syndrome, blood protein disorder; nephritis, at at ataxia telangiectasia; endocaxin lethality; inflammatory bowel disease; histiocytosis; chemotaxis; infectious disease; autoimmune disease; histiocytosis; chemotaxis; infectious disease; autoimmune disease; heurodegenerative disorder; viral infection; poxvirus infection; HUV; human immunodeficiency virus; cytomegalovirus; Kaposi's sarcoma; heumocystis carnii infection; cardiovascular disorder; atherosclerosis;
                                                                                                                                                                                                                    COKEDSVYVCGPYPPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR
                                                                                                                                                                                                                                                                            AVRVI FTIMI VYFLFWIPYNI VILLINI FQEFEGLSNCESTSQLDQATQVIETLGMIHCCI
                                                                                     1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN
                                                                                                                               61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANBWVFGNAMCKLFTGLY
                                                                  Gaps
                                                                ;
                                           Length 374;
                                                               0; Indels
chemokine receptor showing sequence similarity to M/DCCR
                                         ; Score 1970; DB 8;
; Pred. No. 5.1e-215;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Class I receptors WSXWS motif.
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2001US-0297257P.
2001US-0310458P.
2001US-0328447P.
                                           100.0%;
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                                       Query Match
Best Local Similarity 100.0
Matches 374; Conservative
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                      Sequence 374 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lymphocytopenia
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08-AUG-2001;
12-OCT-2001;
21-DEC-2001;
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The invention describes an isolated polynuclectide encoding a first antibody at least 95-100% identical to a second antibody consisting of an antibody at least 95-100% identical to a second antibody consisting of antibody at least 95-100% identical to a second antibody consisting of a variable heavy (VH) or variable light (VL) domain of the antibody expressed by a hybridoma cell line consisting of XF3.5F1, XF11.1F8, XF27.28.3610, XF27.28.3612, XF27.28.361.38.2. The antibody is useful treating, preventing, ameliorating, prognosing or monitoring cancers or other diseases or disorders e.g. immunologic deficiency syndromes such as blood protein disorders e.g. immunologic deficiency syndromes such as blood protein disorders e.g. immunologic deficiency syndromes such as blood protein disorders e.g. immunologic deficiency syndromes such as blood protein disorders e.g. immunologic deficiency syndromes cortain haematopoietic cells such as endotoxin lethality, nephritis and inflammatory bowel disease, conditions associated with an increase in certain haematopoietic cells such as histiocytosis, defective or aberrant chamotaxis of immune cells or T-cell antigen presenting cell interaction, an infection disease, an autoimmune disease such as Addison's disease, disorder, a viral infection e.g. HIV infection, Kaposi's sarcoma, cardiovascular disorders such as atherosclerosis, lymphocytopenias, or a disease or disorder associated with aberrant expression of novel human G-protein chemokine receptor (CCRS) HDGNR10. This is the amino acid sequence of the WSXWS motif found in class I receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DIYLLINIAISDLLFLITLFLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID 120
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                                                                                                                                                                                            New human G-protein Chemokine Receptor gene (HDGNR10) useful for treating, preventing, ameliorating or monitoring diseases or disorders associated with aberrant expression of HDGNR10 e.g. cancer.
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100.0%; Pred. No. 2.5e-198;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                   Example 17; Page 386; 562pp; English.
Ruben SM;
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                                                                                                                                                                                                                                                                                                                           The invention relates to a method of producing an antibody, involving immunising an animal with a human G-protein chemokine receptor (HDCNR10) polypeptide (also referred to as a human 7-transmembrane receptor) and recovering an antibody which binds the polypeptide. The method is useful for producing an antibody which binds specifically to the human G-protein chemokine receptor polypeptide. This sequence represents the monocyte chemoattractant protein 1 (MCP-1) receptor which shares homology with the HDGNR10 polypeptide of the invention
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                                                                                                                                                                                                                                                              with a polypeptide
chemokine receptor
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0
                               Human, G-protein chemokine receptor; receptor; HDGNR10; MCP-1;
7-transmembrane receptor; monocyte chemoattractant protein 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 92.5%; Score 1823; DB 6; Length 344; 100.0%; Pred. No. 2.5e-198; ive 0; Mismatches 0; Indels
           Human monocyte chemoattractant protein 1 (MCP-1) receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Producing an antibody, involves immunizing an animal or with a polypeptide encoded by the human G-protein clone in ATCC 97183, and recovering the antibody.
                                                                                                                                                                                                                                                                                                          Disclosure; Fig 2; 23pp; English
                                                                                                                                                    95US-00466343.
98US-00195662.
99US-00339912.
                                                                                                                                03-SEP-2002; 2002US-00232686
                                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC
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Les 344; Conservative
                                                                                                                                                                                                                                          WPI; 2003-456307/43
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 344 AA;
                                                                                                                                                                                                                     Ruben SM;
                                                                                      JS2003023044-A1
                                                                                                                                                    06-JUN-1995;
18-NOV-1998;
25-JUN-1999;
                                                                 Homo sapiens.
                                                                                                           30-JAN-2003
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ADF72129 standard; protein; 344 AA

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RESULT

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The invention describes a new isolated polymucleotide that encodes an antibody (AB1) comprising an amino acid sequence of at least one, two or three complementarity determining regions (CDR) of a heavy chain variable (VH) domain of an antibody (AB2) that immunospecifically binds to a G-protein chemokine receptor (CTRs), at least one, two or three CDR regions of a light chain varaible (VL) domain of AB2 or at least one, two or three CDR regions of both a VH and a VL domain of AB2. The antibody is useful for detecting, diagnosing, prognosing or monitoring cancers and other hyperproliferating and for treating, preventing or ameliorating a disease or disorder. This is the amino acid sequence of MCP-1, a ligand of human G protein chemokine receptor (CCRS) HDGNRIO.
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                                                                                                                                                                 cytostatic; CCR5 modulator; antibody; G-protein chemokine receptor; CCR5; cancer detection; cancer diagnosis; cancer prognosis; cancer monitoring; cancer; hyperproliferative disorder; human; HDGNR10; ligand; MCP-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 DIYLLNLAISDELFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polypeptide comprising domains of an antibody that binds G-protein chemokine receptor CCR5 is useful to detect, diagnose, prognose or monitor cancers and other hyperproliferative disorders and to treat or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EEVITFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLLLINCKKLKCLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78 DIYLLINLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILLINCKKLKCLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                198 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                          Human G-protein chemokine receptor (CCRS) ligand MCP-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1823; DB 7; I
Pred. No. 2.5e-198;
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100.0%; Pred. No. 2...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 9; 179pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rosen CA, Roschke V, Li Y, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prevent a disease or disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-FEB-2000; 2000US-0181258P.
09-MAR-2000; 2000US-0187999P.
22-SEP-2000; 2000US-0234336P.
09-FEB-2001; 2001US-00779879.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2002; 2002US-00135839.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HUMA-) HUMAN GENOME SCI INC
                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    344; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-898066/82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 344 AA;
                                                                                                                                                                                                                                                                                                                                                     US2003166024-A1
                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                      12-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                           04-SEP-2003
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ADF72129;
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Matches 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
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241 PYNIVILLINTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 300
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  61 DIYLLINLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID 120
                                                                                                                                                                                                                                                                    PYNIVILLATFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immunomodulatory; anticoagulant; antiallergic; immunosuppressive; cytostatic; antiparasitic; infection; leukemia; growth factor activity; T-cell mediated autoimmune disease; psoriasis; allergy; atherogenesis; anaphylaxis; malignancy; inflammation; histamina; igs; silicosis; shock; immunoglobulin B-mediated allergic reaction; rheumatoid arthritis; prostaglandin-independent fever; bone marrow failure; sarcoidosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New human G-protein chemokine receptor polypeptides and polynucleotides, useful for identifying (ant)agonists to the G-protein chemokine receptor
                                                                               181 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT
                                                                                                                                                            WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HDGNR10; human; G-protein chemokine receptor; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                        301 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 344
                                                                                                                                                                                                                                                                                                                                                                       318 IALGCRIAPLOKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hyper-eosinophilic syndrome; vulnerary.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human MCP-1 receptor protein fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 16-17; 22pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB46859 standard; protein; 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95US-00466343.
98US-00195662.
99US-00339912.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (revised)
(first entry)
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RUBEN S M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Li Y, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JS2001000241-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-JUN-1995;
18-NOV-1998;
25-JUN-1999;
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(RUBE/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       wound healing; coagulation; anglogenesis; tumour; chronic infection; leukaemia; T-cell mediated autoimmune diseases; parasitic infection; postrasis; allergy; anaphylaxis; atherogenesis; malignancy; inflammation; prostaglandin-independent fever; bone marrow failure; silicosis; sarcoidosis; rheumatoid arthrits; shock; hyper-eosinophilic syndrome; human; MCP-1 receptor; receptor.
241 PYNIVILLNTRQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a method for screening compounds which bind the G-protein chemokine receptor HDGNR10 (CCR5). Compounds identified by the method of the invention are useful for stimulating haematopolesis, wound healing, cosqulation, angiogenesis, for treating solid tumours, chronic infections, postriasis and for stimulating growth factor activity. The compounds are also useful for treating allergy, anaphylaxis, atterored atterored in the compounds are also useful for treating allergy, anaphylaxis, atterored atterored allergic reactions, prostaglandin-independent fever, bone marrow failure, silicosis, sarcoidosis, rheumatoid arthritis, shock and hyper-eosinophilic syndrome. The present sequence is a human MCP-1 receptor protein. This sequence is used in the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Screening compounds binding to G-protein chemokine receptor HDGNR10, involves contacting test compound with polypeptide of HDGRN10, and observing binding of test compound to polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chemokine receptor; HDGNR10; CCR5; haematopoiesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92.5%; Score 1823; DB 8; Length 344; 100.0%; Pred. No. 2.5e-198; ive 0; Mismatches 0; Indels 0
                                                                               318 IALGCRIAPLOXPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 9; 26pp; English.
                                                                                                                                                                                                                                      ADP86217 standard; protein; 344
                                                                                                                                                                                                                                                                                                                                                                                                   receptor protein.
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Matches 344; Conservative
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18-NOV-1998;
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ADP86217

ADP86217

ADP86217

ADP86217

ADP86217

BE Human

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G-pro

KW Wound

KW Parco

KW Wound

KW Parco

KW Wound

KW Parco

KW Wound

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7-transmembrane receptor; G-protein coupled receptor; GPCR; HDGNR10; G-protein chemckine receptor; haematopoletic; immunosuppressant; antiparasitic; antipacitatic; antiallergic; antiinflammatory; cytostatic; antirheumatic; antiathritic; gene therapy; human; MCP-1; receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DIYLLNLAISDLIFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           258 PYNIVILLINTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPLIYAFVGEKFRSLFH 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    226 PYNIVILLINTEQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 285
activity and can be used for gene therapy. The G-protein chemokine receptors, HDGNR10, (I) are useful for screening for compounds which activate or inhibit activation of (I). The products of the invention can also be used for stimulating haematopoiesis, wound healing, coagulation, angiogenesis, treating solid tumours, chronic infections, leukemia, T-cell mediated autoimmune diseases, parasitic infections, psoriasis, antimulating growth factor activity. HDGNR10 is useful for treating allergy, atherogenesis, anaphylaxis, malignancy, chronic and acute inflammation, histamine and immunoglobulin B (IgB)-mediated allergic reactions, prostaglandin-independent fever, bone marrow failure, sillicosis, sarcoidosis, rheumatoid arthritis, shock and hyperecsinophilic syndrome. (N.B. This record was resubmitted to correct errors in the keyword formatting)
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                                                                                                                                                                                                                                                                                                                         Match 87.7%; Score 1727.5; DB 4; Length 329; Local Similarity 95.6%; Pred. No. 1.8e-187; e8 329; Conservative 0; Mismatches 0; Indels 15;
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(RUBE/) RUBEN S M.
                                                                                                                                                                                                                                                                                      Sequence 329 AA;
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                                                                                                                                                                          The invention relates to a novel human 7-transmembrane receptor, HDGNR10, which has been identified as a G-protein chemokine receptor. The GPCR HDGNR10 polypeptide can be expressed by standard recombinant methodology. Compounds that activate or inhibit the receptor polypeptide, optionally expressed from DNA in gene therapy vectors, are used to treat diseases that require: (a) activation of the receptor (e.g. stimulation of harmatopoiesis, treatment of solid tumours, T-cell mediated autoimmune diseases, parasitic infections, psoriasis etc.); or (b) inhibition of the receptor (e.g. allergy, inflammation, rheumatoid arthritis, silicosis etc.) The present sequence represents a human MCP-1 receptor used in comparison studies with the HDGNR10 receptor
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                                                                              New polynucleotide encoding a human G protein chemokine receptor HDGNR10,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87.7%; Score 1727.5; DB 595.6%; Pred. No. 1.8e-187; tive 0; Mismatches 0;
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                                        WPI; 2002-598724/64.
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Li Y, Ruben SM;
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The invention provides a human G-protein chemokine receptor (CCR5) HDGNR10 polymucleotide, polypeptides, and antibodies. The antibody that is an antagonist of HDGNR10 is potentially useful for preventing or treating allergy, atherogenesis, anapylaxis, malignancy, chronic and acute inflammation, histamine and IgB-mediated allergic reactions, prostaglandin-independent fever, bone marrow failure, silicosis, rheumatoid arthritis, shock and hypereosinophilic syndrome. The compounds that bind to and activate the receptor are potentially useful for stimulating haematopoiesis, wund healing, coagulation and angiogenesis, and in treating solid tumours, chronic infections, peoriasis. The antibody may also be used as a diagnostic reagent. The present sequence is a human MCP-1 receptor fragmostic reagent. The present sequence is a human MCP-1 receptor fragmostic reagent. The present sequence is a human MCP-1 receptor fragmostic reagent. The present sequence is a human MCP-1 receptor fragmostic reagent. The present sequence is a human MCP-1 receptor fragmostic reagent. The present sequence is a human MCP-1 receptor fragmostic reagent. The present sequence is a human MCP-1 receptor fragmostic reagent. The present sequence is a human MCP-1 receptor fragmostic reagent. The present sequence is a human MCP-1 receptor fragmostic reagent. The month of the man MCP-1 receptor fragmostic reagent. The month of the man MCP-1 receptor fragmostic reagent. The month of the man MCP-1 receptor fragment (CCR5)
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                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated antibody that binds to an extracellular portion of human G-protein chemokine receptor 5 (CCR5) (also known as HDGNR10), useful for treating conditions such as allergies, cancers, and inflammation.
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                                                                                                                     06-JUN-1995; 95US-00466343.
18-JUN-1998; 98US-00195662.
25-JUN-1999; 99US-0039912.
11-FEB-2000; 2000US-00502783.
23-APR-2002; 2002US-00127764.
                                                                        04-MAR-2004; 2004US-00791905.
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Matches 329; Conservative
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Compugen Ltd.
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  GenCore version
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	31	484	24.6	350	7	JN0621		G prot	G protein-coupled	ğ	
	32	480	24.4	359	N	A42656		angiot	ensin II	rec	
	33	479.5	24.3	374	~	842628		G prot	protein-coupled	ď	
	34	475	24.1	359	N	151372		angiotensin	Η	rec	
	35	473	24.0	359	~	JC2134		angiotensin	Η	rec	
	36	472	24.0	359	~	JH0621		angiotensin	II	Sec.	
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	42	465	23.6	374	N.	S32785		G prot	G protein-coupled	ਯੂ	
	43	464	23.6	359	N	A48857		angiot	angiotensin II r	rec	
	44	461.5	23.4	372	N	S26667		G profe	protein-coupled	70	
	45	460.5	23.4	327	0	856162		MDCR15	MDCR15 protein -	ч	
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	N;Altern	ate name	ე-ე :ga	CKR-2;	Ë	N,Alternate names: C-C CKR-2; monocyte chemoattractant protein 1	ttractant	rotein 1	receptor; monocyte	monocyte chemo	SEC.
	C; Specie	B: Homo	sapien	(man)							
	C;Date:	16-FeD-,	1996 #8	equence	ıre	C;Date: 16-Feb-1996 #Sequence_revision 16-Feb-1996 #text	-1996 #rext	_cnange	09-Jul-2004		
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	A; Title:	Molecu	lar clo	ning an	, A	unctional exp	ression of	two monocyte chemoattractant	rte chemoa		prot
	A; Refere	nce num	ber: A5	3477; M	II	:94195821; PM	ID:8146186				
	A; Access	ion: 138	3450			•					
	A;Status	: prelin	ninary								
	A; Molecu	le type:	: mRNA								
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	A, Cross-	referen	ces: UN	I PROT: F	415	Cross-references: UNIPROT:P41597; EMBL:U03882; NID:g47255	82; NID:94	 	PIDN: AAA19119	.1; PID:9472	255
	C;Geneti	C8:	,								
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	A;Cross-	rereren	ביים ביים	5:33/36		GDE:33/364; UMIM:60126/					
	A; Map po	BILION:	3p21-3	pzi	1	1					
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181 181

HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK

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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 12-101-1996 #sequence revision 12-Jul-1996 #text_change 20-Jun-2000
C;Date: 12-Jul-1996 #sequence revision 12-Jul-1996 #text_change 20-Jun-2000
C;Accession: A41113; S71808; A58834; A58832; G02653; A58833
R;Samson, M; Labbe, O; Mollereau, C.; Vassart, G.; Parmentier, M.
Biochemistry 35, 3362-3367, 1996
A;Title: Molecular cloning and functional expression of a new human CC-chemokine receptor A;Reference number: A43113; MUID:96241590; PMID:8639485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-352 <SAM1-
A; Residues: 1-352 <SAM1-
A; Cross-references: GB:X91492; NID:g1262810; FIDN:CAA62796.1; FID:g1262811
A; Cross-references: GB:X91492; NID:g1262810; Filesnard, C.; Farber, C.M.; Saragost;
M.; Imai, T.; Rana, S.; Yi, Y.; Smyth, R.J.; Collman, R.G.; Doms, R.W.; Vassart, G.; Pan
Nature 382, 722-725, 1996
A; Title: Resistance to HIV-1 infection in caucasian individuals bearing mutant alleles of
A; Reference number: S71808
A; Reference number: S71808
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Accession: A58834
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Ancession: A58834
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Nolecule type: DNA
A;Residues: 1-184, 'IXOSHLGAGPPAAACHGHLLLGNPKNSASVSK' <SAM3>
A;Cross-references: GB:X99393; NID:g1524062; PIDN:CAA67767.1; PID:g1524063
A;Note: this frameshift mutation results in a non-functional receptor but confers a degree of may have had a selective advantage by conferring resistance to Yersinia plague infecti R;Combadiere, C; Ahuja, S.K.; Tiffany, H.L.; Murphy, P.M.
J. Leukoc. Biol. 60, 147-152, 1996
A;Rifle: Cloning and functional expression of CC CKRS, a human monocyte CC chemokine rece A;Reference number: A58832; MUID:96295970; PMID:8699119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross references: GB:U54994; NID:g1457945; PIDN:AAC50598.1; PID:g1457946
C;Comment: This is a receptor for chemokines MIP-1alpha (see PIR:A30574), MIP-1beta (see
C;Comment: Macrophage- and dual-tropic strains of HIV-1 bind to a complex of chemokine (C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Accession: G02653
A;Status: translated from GB/EMBL/DDBJ
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-89,'L', 91-352 «COM2»
A;Cross-references: EMBL:U57840
B;Raport, C.J.; Gosling, J.; Schweickart, V.L.; Gray, P.W.; Charo, I.F.
A;Title: Molecular cloning and functional characterization of a novel human CC chemokine
A;Reference number: A58833; MUID:96291862; PMID:8663314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: nucleic acid sequence not shown; not compared with conceptual translation A;Molecule type: DNA
A;Residues: 182-206;207-230 <SAM2>
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A;Residuse: 1-52 < COND.
A;Cosa-references: GB:U57840; NID:g1502408; PIDN:AAB17071.1; PID:g1502409
A;Experimental source: clone 8, endotoxin-stimulated peripheral blood monocytes
                                             241 AVRVIPTIMIVYPLFWTPYNIVILLINTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
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A,Cross-references: GDB:1230510; OMIM:601373
A,Map position: 3p21-3p21
                                                                                                                                                       301 NPIIYAFVGEKFR---SLF---HIALG-CRIAPL 327
                                                                                                                                                                                                301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPV 334
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                                                                                                                                                                                                                                                                                                                                                                                                                                 chemokine (C-C) receptor 5 - human N;Alternate names: C-C CKR-5; CCR5
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A;Residues: 1-352 <RAP>
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C; Superfamily: vertebrate rhodopsin
C; Superfamily: vertebrate rhodopsin
C; Superfamily: vertebrate rhodopsin
C; Superfamily: vertebrate rhodopsin
C; Superfamily: vertebrate splicing of protein-coupled receptor; glycoprotein; transmembrane #status predicted <TM1>
F; 813-70/Domain: transmembrane #status predicted <TM2>
F; 815-31/Domain: transmembrane #status predicted <TM3>
F; 815-41/B/Domain: transmembrane #status predicted <TM4>
F; 8207-226/Domain: transmembrane #status predicted <TM6>
F; 8207-226/Domain: transmembrane #status predicted <TM6>
F; 8207-209/Domain: transmembrane #status predicted <TM6>
F; 814-26B/Domain: transmembrane #status predicted <TM6>
F; 814-190/Domain: transmembrane #status predicted <TM7>
F; 811-190/Domain: transmembrane #status predicted <TM7>
F; 811-190/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Accession: JC2443
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Rossiues: 1-560 «YMA>
A;Cross-references: UNIPROT:P41597; DDBJ:D29984; NID:g531246; PIDN:BAA06253.1; PID:g5312
R;Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.
B;Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.
A;Title: Molecular cloning and functional expression of two monocyte chemoattractant pro
A;Reference number: A53477; MUID:94195821; PMID:8146186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chemokine (C-C) receptor 2, splice form B - human
Altlernate names: C-C (2RR-2; monocyte chemoattractant protein 1 receptor; monocyte chem
C;Species: Homo sapiens (man)
C;Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 09-Jul-2004
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R;Yamagami, S.; Tokuda, Y.; Ishii, K.; Tanaka, H.; Endo, N.
Biochem. Biophys. Res. Commun. 202, 1156-1162, 1994
A;Title: CDNA cloning and functional expression of a human monocyte chemoattractant A;Reference number: JC2443; MUID:94324942; PMID:8048929
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                                                                                                                                                       301 NPIIYAFVGEKFRSLFHIALGCRIAPLOKPVCGGPGVRPGKNVKVTTOGLLDGRGKGKSI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :Cross-references: EMBL:U03905; NID:g472557; PIDN:AAA19120.1; PID:g472558
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                                                                                                                                                                                                                                                                                                                   361 GRAPEASLQDKEGA 374
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A;Residues: 1-360 <RES>
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A;Map position: 3p21-3p21
C;Superfamily: vertebrate rhodopsin
C;Superfamily: vertebrate rhodopsin
C;Keywords: disulfide bond; G protein-coupled receptor; glycoprotein; phosphoprotein; tre
F;36-60/Domain: transmembrane #status predicted <TM1>
F;71-91/Domain: transmembrane #status predicted <TM2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 RLKAMTSIYLLANLAISDLLFLFTLPFWIDYKLKDDWVFGDAMCKILSGFYYTGLYSEIFF 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVC 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        191 GPYFP----RGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIF 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      247 TIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYA 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 243 VIMIIFFLFWTPYNLTILISVFQDFLFTHECEQSRHLDLAVQVTEVIAYTHCCVNPVIYA 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAA-NEWVFGNAMCKLFTGLYHIGYFGGI 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 NTTED-YDTTTEFDYGDATPCQXVNERAFGAQLLPPLYSLVFVIGLVGNILVVLVLVQYK 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of three mouse
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C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCK
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C;Superfamily: vertebrate rhodopsin
                                                                                                                                                                                                                       Fil08-129/Domain: transmembrane #status predicted <TM3>
Fil7-171/Domain: transmembrane #status predicted <TM4>
Fi205-223/Domain: transmembrane #status predicted <TM5>
Fi206-223/Domain: transmembrane #status predicted <TM5>
Fi208-305/Domain: transmembrane #status predicted <TM7>
Fi5/Binding site: carbobydrate (Asn) (covalent) #status predicted Fi24-273,106-183/Disulfide bonds: #status predicted Fi24-273,106-183/Disulfide Fi24-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 967.5; DB 2; Length 3
Pred. No. 4.9e-77;
47; Mismatches 72; Indels
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R,Gao, J.L.; Murphy, P.M.
J. Biol. Chem. 270, 17494-17501, 1995
A;Title: Cloning and differential tissue-specific expression A;Reference number: 149339; MUID:95340546; PMID:7542241
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Local Similarity 50.1%; Pred. No. 2.2e-76;
Les 187; Conservative 59; Mismatches 89;
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   GDB:138446; OMIM:601159
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Best Local Similarity 58.7
Matches 185; Conservative
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Best Local S:
Matches 187
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R;Necte, K.; DiGregorio, D.; Mak, J.Y.; Horuk, R.; Schall, T.J.
R;Necte, K.; DiGregorio, D.; Mak, J.Y.; Horuk, R.; Schall, T.J.
A;Title: Molecular cloning, functional expression, and signaling characteristics of a C-A;Reference number: A45177; MUID:93161416; PMID:7679328
                                                                  C;Keywords: AIDS; G protein-coupled receptor; glycoprotein; phosphoprotein; transmembran #812-56/Domain: transmembrane #status predicted <TM1>
F;32-56/Domain: transmembrane #status predicted <TM2>
F;03-124/Domain: transmembrane #status predicted <TM3>
F;103-124/Domain: transmembrane #status predicted <TM3>
F;103-128/Domain: transmembrane #status predicted <TM4>
F;193-218/Domain: transmembrane #status predicted <TM5>
F;20-250/Domain: transmembrane #status predicted <TM5>
F;20-269,101-178/Disulfide bonds: #status predicted <TM7>
F;20-269,101-178/Disulfide bonds: #status predicted 
F;268-300/Domain: transmembrane #status predicted <TM7>
F;20-269,101-178/Disulfide bonds: #status predicted 
F;268-317,342/Binding site: carbohydrate (Ser) (covalent) #status predicted
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A;Experimental source: HL60 cells
A;Note: sequence extracted from NCBI backbone (NCBIP:124876)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A:Title: Structure and functional expression of the human macrophage inflammatory 1 alph
A;Reference number: 155671; MUID:93240122; PMID:7683036
A;Accession: 155671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ë
A;Note: probably acts to control granulocyte proliferation and differentiation C;Superfamily: vertebrate rhodopsin
C;Keywords: AIDS; G protein-coupled receptor; glycoprotein; phosphoprotein; tra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NiAlternate names: C-C CKR-1; macrophage inflammatory protein-1-alpha receptor C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PYNIVILLINTFORFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLF- 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PYNIVILLATFQEFFGLANCSSSNRLDQAMQVTETLGATHCCINPIIYAFVGEKFRAYLL 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLA 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 YDINYYTSBPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILLLINCKRLKSMTDIYL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FDYDY -- GAPCHKFDVKOIGAOLLPPLYSLVPIFGFVGNMLVVLILINCKKLKCLTDIYL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;340,343/Binding site: phosphate (Thr) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 1224; DB 2;
; Pred. No. 1.8e-99;
27; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62.1%;
ilarity 76.3%;
Conservative 2'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----HIA 319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 310 VPFQKHIA 317
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Best Local Similarity
Matches 235; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Residues: 1-355 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
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A,Residues: 1f..., 106,'N', 108-275,'S',277-280,'R',282-355 <COM>
A,Cross-references: GB:U28694; NID:g1199579; PIDN:AAC50469.1; PID:g1199580
A,Note: the translated sequence in GenBank entry HSU28694, release 113.0, PIDN:AAC50469.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A Map position: 3p21-3p21
C;Superfamily: vortebrate rhodopsin
C;Superfamily: vortebrate rhodopsin
C;Superfamily: vortebrate rhodopsin
C;Reywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane #status predicted <TM1>
F;36-60/Domain: transmembrane #status predicted <TM2>
F;71-91/Domain: transmembrane #status predicted <TM3>
F;105-125/Domain: transmembrane #status predicted <TM4>
F;47-171/Domain: transmembrane #status predicted <TM5>
F;205-223/Domain: transmembrane #status predicted <TM5>
F;205-223/Domain: transmembrane #status predicted <TM6>
F;240-261/Domain: transmembrane #status predicted <TM6>
F;240-261/Domain:
                                                                                        A;Reference number: H01272
A;Reference number: H01272
A;Raccession: G02436
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-355 < PON>
A;Residues: 1-355 < PON>
A;Cossa-references: UNIPROT:P51677; EMBL:U49727; NID:g1477560; PIDN:AAB09726.1; PID:g1477
B;Combadiere, C:, Ahuja, S.K.; Murzphy, P.M.
J. Biol. Chem. 270, 16491-16494, 1995
A;Title: Cloning and functional expression of a human eosinophil CC chemokine receptor.
A;Reference number: A57237; MUID:95348056; PMID:7622448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;288-305/Donain: transmembrane #status predicted <TM7>
F;24-273,106-183/Disulfide bonds: #status predicted
F;345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chemokine (C-C) receptor 4 - mouse
chamokine (C-C) was musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 08-Mar-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
C;Accession: JC4587
R;Hoogewerf, A.J.; Black, D.; Proudfoot, A.E.I.; Wells, T.N.C.; Power, C.A.
B;Hoogewerf, A.J.; Black, D.; Proudfoot, A.E.I.; Wells, T.N.C.; Power, C.A.
Biochem. Biophys. Res. Commun. 218, 337-343, 1996
A;Title: Molecular cloning of murine CC CKR-4 and high affinity binding of chemokines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LAIVHAVFALKARIVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPR--- 196
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45.2%; Score 890.5; DB 2; Length 355;
Best Local Similarity 54.6%; Pred. No. 2.7e-70;
Matches 167; Conservative 56; Mismatches 72; Indels 11
                               R;Ponath, P.D. submitted to the EMBL Data Library, February 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: GDB:579624; OMIM:601268
                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Accession: A57237
A;Status: nucleic acid sequence not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
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Superfamily: vertebrate rhodopsin
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                                                                                                                                                                                                                                                                                                            245 IFVVMIVPFIFWTPYNLVLLFSAFHSTPLETSCEQSKHLDLAMQVTEVIAYTHCCVNPVI 304
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                                                                                                                                                                      186 SCSPRYPEGEEDSWKRFHALRANIFGLALPLLVAVICYSGIIKTLLRCPN-KKKHKAIRL 244
                                                                                                                                                                                                                                                                         IFTIMIVYFLFWTPYNIVILLINTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINFII 304
                                                                                                                                                                                                                                                                                                                                                                                                            YAFVGEKFRS----LFHIALGCRIAPLOKPVCGGPGVRPGKNVKVTTQGL---LDGRGKG 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFP---- 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72
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N;Alternate names: C-C CKR-3
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
                                   126 FFIILTIDRYLAIVHAVFALRARTVTFATITSIITWGLAGLABEPIFHESQDSFGEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  189 VCGPYFPRG----WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ------RNVQFTWENIFQFLPGEENG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WIPYNLSVFVSAFODVLFTNQCEQSKHLDLAMQVIEVIAYTHCCVNPIIYVFVGERFWKY
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R;Gao, J.L.; Murphy, P.M.
J. Biol. Chem. 270, 17494-17501, 1995
A;Title: Cloning and differential tissue-specific expression of three A;Reference number: I49339; MUID:95340546; PMID:7542241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 355;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         macrophage inflammatory protein-1 alpha receptor - mouse C;Species: Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45.8%; Score 902.5; DB 2; 53.1%; Pred. No. 2.4e-71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 45.8%; Score 902.5; Best Local Similarity 53.1%; Pred. No. 2.4e Matches 170; Conservative 58; Mismatches
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LRQLFQRHVAI-----PLAK 326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   358 KSIGRAPEASLQD 370
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RTSSVSPSTGEQE 354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Molecule type: DNA
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Query Match 40.3
Best Local Similarity 44.3
Matches 164; Conservative
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                                                                                                                                                      Best Local Simi
Matches 154;
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                                                                                                                                    Query Match
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P;76-97/Domain: transmembrane #status predicted <TM2>
P;12-133/Domain: transmembrane #status predicted <TM3>
P;112-175/Domain: transmembrane #status predicted <TM4>
F;208-226/Domain: transmembrane #status predicted <TM6>
F;208-226/Domain: transmembrane #status predicted <TM6>
F;243-264/Domain: transmembrane #status predicted <TM6>
                                                                    A; Cross-references: UNIPROT: P51679; GB: X85740; NID: 91370103; PIDN: CAA59743.1; PID: 997145
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R;Power, C.A.; Meyer, A.; Nemeth, K.; Bacon, K.B.; Hoogewerf, A.J.; Proudfoot, A.E.I.;
J. Biol. Chem. 270, 19495-19500, 1995
A;Title: Molecular cloning and functional expression of a novel CC chemokine receptor of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVY 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIY 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69 NCKKCKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGI 128
                                                                                                                                                                                                                                                                                                                                                                  10 IRNTNESGEEVTTFFDYD-YGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILLI 68
                                                                                                                                                                                                                                                                                                                                                                                                      VIDITODETVYNSYYFYESMPKPCTKEGIKARGEVFLPPLYSLVFLLGLFGNSVVVLVLF 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Homo sapiens (man)
C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YCKTQYSVNSTTWKVLSSLEINVLGLLIPLGIMLFWYSMIIRTLQHCKNEKK-NRAVRMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    189 VCGPYF---PRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVI
                                                                                                                                                                                                                                                                                                                              22; Gaps
                                                                                                                                                                                                                                                                                                Pred. No. 2.9e-65;
M. smatches 89; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary; not compared with conceptual translation
A;Reference number: JC4587; MUID:96136324; PMID:8573157
A;Accession: JC4587
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            306 AFVGEKFR----SLFHIALGCRIAPLQKPVCGGP 335
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                                                                                                                                                                                                                                                                                                                            63; Mismatches
                                                                                                                                                                                                                                                                                      42.3%; Score 833;
47.9%; Pred. No. 2
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C;Superfamily: vertebrate rhodopsin
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FFLGEKFRKYITQLFR----
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                                                                                                                                                                                                                                                                                                                            Matches 160; Conservative
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                                                        A; Residues: 1-360 <HOO>
                                                                                                                                                                                                                                                                                                        Best Local Similarity
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                                      mRNA
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F;291-308/Domain: transmembrane #status predicted <TW7>
F;29-276,110-187/Disulfide bonds: #status predicted
F;22-376,110-187/Disulfide bonds: #status predicted
F;72,350/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F;145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F;183,194/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
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A, Residues: 1-383 <TEL>
A, Cross-references: UNIPROT.Q89609, GB:U20824; NID:g695172; PIDN:AAC13788.1; PID:g695173
C,Superfamily: vertebrate rhodopsin
C,Keywords: G protein-coupled receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    151 ARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG---WNNFHTIMRN 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWTPYNIVILLNT 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 LVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAH--SAANEWVFGNAMCKLFTGL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YHIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KKRHRAVRVIPTIMIVYFLFWTPYNIVILLINTFQEFFGLSNCESTSQLDQATQVTETLGM 295
                                                                                                                                                                                                                                                                                                                                                                                                                                       87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         268 FQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRS-LFHIALGCR 323
                                                                                                                                                                                                                                                                                                                                                                                                               28 PCTKEGIKARGELFLPPLYSLVFVPGLLGNSVVVLVLFKYKRLRSMTDVYLLNLAISDLL
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                                                                                                                                                                                                                                                                                                                                                                            PCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIYLLNLAISDLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G protein-coupled receptor B1 - equine herpesvirus 2
C;Species: equine herpesvirus 2
C;Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul
C;Accession: 855594
R;Telford, B.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.
J. Mol. Biol. 249, 520-528, 1995
A;Title: The DNA sequence of equine herpesvirus 2.
A;Reference number: 855594; MUID:95302501; PMID:7783207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39;
                                                                                                                                                                                                                                          DB 2; Length 360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 383;
                                                                                                                                                                                                                                                                      ..9e-65;
les 80; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40.3%; Score 794.5; DB 2; Length 44.3%; Pred. No. 7.2e-62; ive 60; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; nucleic acid sequence not shown
                                                                                                                                                                                                                                       42.2%; Score 831.5;
51.9%; Pred. No. 3.9e
tive 58; Mismatches
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A;Cross-references: UNIPROT:P35411; EMBL:U04808; NID:g2558635; PIDN:AAB87093.1; PID:g4398
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: IS8186
R;Harrison, J.K.; Barber, C.M.; Lynch, K.R.
R;Harrison, J.K.; Barber, C.M.; Lynch, K.R.
Neurosci. Lett. 169, 85-89, 198,
A;Title: cDNA cloning of a G-protein-coupled receptor expressed in rat spinal cord and A;Reference number: IS8186
A;Accession: IS8186
A;Accession: IS8186
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-354 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69 ITDVYLLNLALSDLLFVFSFPFQTYYLLDQWVFGTVMCKVVSGFYYIGFYSSMFFITLMS 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        129 VDRYLAVVHAVYALKVRTIRMGTTLCLAVWLTAIMATIPLLVFYQVASEDGVLQCYSFYN 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      248 ILFWVPRNVVLFITSLHSMHILDGCSISQQLTYATHVTBIISFTHCCVNPVIYAFVGEKF 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   136 IDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFP 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         196 R---GWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVY 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probable G protein-coupled receptor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 VITVIDYYYPDIFSSPCDABLIQINGKLLLAVFYCLLFVFSLLGNSLVILVLVVCKKLRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              253 FLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 VITEPDYDY ----GAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76 LTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLT
                                                                                                                                                                                                                                    A;Residues: 1-355 <BON>
A;Cross-references: EMBL:U45983; NID:g1245056; PID:g1245057
C;Comment: This protein belongs to the family of beta chemokine receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                A;Genera GDB:CMKBRB; CMKBRL2; TER1; CKR-L1
A;Gross-references: GDB:6053733; OMIM:601834
A;Cross-references: GDB:6053733; OMIM:601834
C;Superfamily: vertebrate rhodopsin
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein
C;Keywords: G protein-coupled receptor; transmembrane protein
C;Keywords: G protein-coupled receptor; transmembrane protein
C;Keywords: G protein-coupled receptor; transmembrane #status predicted cTM1>
F;73-94/Domain: transmembrane #status predicted cTM3>
F;100-222/Domain: transmembrane #status predicted cTM5>
F;200-222/Domain: transmembrane #status predicted cTM6>
F;21-304/Domain: transmembrane #status predicted cTM6>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36.7%; Score 723; DB 2; Length 355; 43.5%; Pred. No. 1.2e-55; rative 59; Mismatches 103; Indels
                        A;Cross-references: EMBL:U62556; NID:g1468978; PID:g1468979
                                                                                                                              A; Accession: GG2387
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
                                                       R;Bonner, T.I. submitted to the EMBL Data Library, January 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 131; Conservative
                                                                                                                     A; Reference number: H01154
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A; Residues: 1-355 < NAP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              308 K 308
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                                                                                                                                                                                                                                                                                                                                 Genetics:
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                                                                                                                                                                                                                                                                                                                                                                               C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: 149340
C;Accession: 149340
J; Murphy, P.M.
J; Murphy, P.M.
J; Biol. Chem. 270, 17494-17501, 1995
A;Title: Cloning and differential tissue-specific expression of three mouse beta chemoki
A;Reference number: 149339; MUID:95340546; PMID:7542241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:P51685; EMBL:Z79782; NID:91668735; PIDN:CAB02142.1; PID:9166 R;Napolitano, M.; Zingoni, A.; Bernardini, G.; Spinetti, G.; Rocchi, M.; Santoni, A. submitted to the EMBL Data Library, June 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cross-references: UNIPROT:P51676; EMBL:U28405; NID:9881549; PIDN:AAA89154.1; PID:98819
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C; Species: Homo saptens (man)
C; Species: Homo saptens (man)
C; Date: 31-Jan-1997 #sequence revision 31-Jan-1997 #text_change 09-Jul-2004
C; Datession: JC5067; G02776; G02387
R; Zaballos, A.; Varona, R.; Gutierrez, J.; Lind, P.; Marquez, G.
Biochem: Biochem. 227, 846-853, 1996
A; Title: Molecular cloning and RNA expression of two new human chemokine receptor-like A; Reference number: JC5067; MUID:97040707; PMID:8886020
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       144 HAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPR----GWN 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      200 NFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWTPY 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AISDLLFLITLPLWA-HSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLAIV 143
                              296 THCCINPIIYAFVGEKFR----SLFHIALG---CRIAPLOKPVCGGPGVRPGKNVKVTTQ 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 198 RFQALTMNILGLILPLLAMIICYTRIINVLHR-RPNKKKAKVWRLIFVITLLFFILLAPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25 DYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIYLLNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 37.1%; Score 731; DB 2; Length 35 Best Local Similarity 46.6%; Pred. No. 2.4e-56; Matches 137; Conservative 59; Mismatches 92; Indels
                                                                   331 THCCINPVIYAFVGEKFRRHLYHFFHTYVAIYLCKYIP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Accession: 149340
A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                   - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Superfamily: vertebrate rhodopsin
                                                                                                                                                    349 GLLDGRGKGK 358
                                                                                                                                                                                                           369 -FLSGDGEGK 377
                                                                                                                                                                                                                                                                                                                                                             MIP-1 alpha receptor like-1
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A, Molecule type: DNA
A, Residues: 1-355 < ZAB>
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A, Cross-references: UNIE
C, Superfamily: vertebrat
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A;Residues: 1-344 <FAN>
A;Cross-references: UNIPROT:000421; GB:U97123; NID:g2897070; PIDN:AAC39595.1; PID:g289707
C;Superfamily: vertebrate rhodopsin
                                                                        VLQEIWPVLRNVETNFLGFLLFPLLIMSYCYFRIIQTLFSCKNHKKA-KAIKLILLVVIVF 240
                                                                                                                                                                     241 FLFWTPYNVMIFLETLKLYDFFPSCDMRKDLRLALSVTETVAFSHCCLNPLIYAFAGEKF 300
                                                197 GWNNFHTIMRNI----LGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVY 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87 SDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLAIVH-A 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          146 VPALKARIVIFGVVTSVIIWLVAVFASVPGIIFTKCQKEDSVYVCG----PYFPRG---W 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YNIVILINTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRS---- 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          126 DRYLAIVLAANSMINRTVQHGVTISLGVWAAAILVAAPQFMFTK-QKENE---CLGDYPE 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23 DEAEQCDKYDAQALSAQLVPSLCSAVFVIGVLDNLLVVLILVKYKGLKRVENIYLLNLAV 82
                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Homo sapiens (man)
C;Bate: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Bate: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Bate: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
R;Fan, P.; Kyaw, H.; Su, K.; Zeng, Z.; Augustus, M.; Carter, K.C.; Li, Y.
Biochem. Biophys. Res. Commun. 243, 264-268, 1998
Biochem. Biophys. Res. Commun. 243, 264-268, 1998
A;Title: Cloning and characterization of a novel human chemokine receptor.
A;Reference number: JC5942; MUID:98139902; PMID:9473515
                                                                                                                                        FLFWTPYNIVILLNTFQBFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   199 NNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27 DYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIYLLNLAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32.7%; Score 644.5; DB 2;
39.9%; Pred. No. 8.7e-49;
live 58; Mismatches 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            315 LFHIALGCRIAPLQKPVCGGPGVRPGKNVKV 345
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                                                                                                                                                                                                                                    RS-LFHIALGCRIAPLQKPVCG 333
                                                                                                                                                                                                                                                                                301 RRYLYHLYGKCLAV----LCG 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 39.94
Matches 132; Conservative
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Croment: This protein is a cell-surface receptor which recognizes extracellular signal
Comment: This protein is a key regulator of many immune and homeostatic responses, and
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Astricle: The orphan G-protein-coupled receptor-encoding gene V28 is closely related A, Reference number: JC4304; MUID:96011651; PMID:7590284
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C.Species: Homo sapiens (man)
C.Date: 16-Nov-1995 #sequence_revision 08-Peb-1996 #text_change 09-Jul-2004
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C;Superfamily: vertebrate rhodopsin
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F;Seyvords: G protein-coupled receptor; lymphokine; transmembrane #status predicted <TM1>
F;66-88/Domain: transmembrane #status predicted <TM2>
F;104-125/Domain: transmembrane #status predicted <TM3>
F;146-165/Domain: transmembrane #status predicted <TM5>
F;197-217/Domain: transmembrane #status predicted <TM5>
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Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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SEQUENCE FROM N.A., AND VARIANTS ILE.64 AND GLU-355.
Rieder M.J., Armel T.Z., Carrington D.P., Ozuna M., Kuldanek S.A., Asalkumar N., Toth E.J., Yi Q., Nickerson D.A.;
"SeattleSNPs. NHLBI Hic6682 program for genomic applications, UW-FHCRC, Seattle, WA (URL: http://pga.gs.washington.edu).";
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Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO: 00105887; C:integral to plasma membrane; TAS.
GO: 00105887; C:integral to plasma membrane; TAS.
GO: 00109525; C:solubble fraction; TAS.
GO; GO:0004550; P:chemokine receptor activity; TAS.
GO; GO:0019735; P:chemokine response; TAS.
GO; GO:0006958; P:chemokial humoral response; TAS.
GO; GO:0006959; P:chemokiaxis; TAS.
GO; GO:0007204; P:cytosolic calcium ion concentration elevation; TAS.
GO; GO:0007204; P:inflammatory response; TAS.
GO; GO:0007194; P:inflammatory response; TAS.
InterPro; IPR002237; CC_2 receptor.
InterPro; IPR000355; ChmkIne_receptor.
InterPro; IPR000376; GPCR_Rhodpsn.
                                                                                          Preobrazhensky A.A., Dragan S., Kawano T., Gavrilin M.A., Gulina I.V., Chakravarty L., Kolattukudy P.E.; "Monocyte chemoractic protein-1 receptor CCR2B is a glycoprotein that has tyrosine sulfation in a conserved extracellular N-terminal
                                                                                                                                                                                        region.";
J. Immunol. 165:5295-5303(2000).

-!- FUNCTION: Receptor for the MCP-1, MCP-3 and MCP-4 chemokines.

-!- FUNCTION: Receptor for the MCP-1, MCP-3 and MCP-4 chemokines.

Transduces a signal by increasing the intracellular calcium ions level. Alternative coreceptor with CD4 for HIV-1 infection.

-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R PERINTS; PRODO1; 7tm 1; 1.

R PRINTS; PRODO1; 7tm 1; 1.

R PRINTS; PRODO27; GFCRHODOPSN.

R PROSITE; PSO0237; GFCRTEN RECEP F1 1; 1.

DR PROSITE; PSO0262; G-PROTEIN RECEP F1 2; 1.

KW 3D-SETUCLURE, Alternative splicing; G-protein coupled receptor; KW Glycoprotein; Polymorphism; Sulfation; Transmembrane.

FT TRANSMEM 43 70 1 (Potential).

FT TRANSMEM 81 100 2 (Potential).

FT TRANSMEM 81 100 2 (Potential).

FT TRANSMEM 115 136 3 (Potential).

FT TRANSMEM 137 153 Cytoplasmic (Potential).

FT TRANSMEM 154 178 4 (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i- PTM: N-glycosylated.
-i- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
    Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                          Event_Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       [Bold=P41597-2; Sequence=VSP_001893;
                                                                                                                                                                                                                                                                                                                                                                                                           IsoId=P41597-1; Sequence=Displayed;
                                                 SULFATION OF TYR-26, AND N-GLYCOSYLATION MEDLINE=20501139; PubMed=11046064;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U03882; AAA19119.1; --
EMBL; U03905; AAA19120.1; --
EMBL; U03905; AAA19120.1; --
EMBL; U80924; AAC51637.1; --
EMBL; U95626; AAB57791.1; --
EMBL; U95626; AAB57791.1; --
EMBL; U95626; AAB57791.1; --
EMBL; AF545480; AAN16400.1; --
PIR; J38450; I38450.
PDB; IKAD; Model; A=1-349.
PDB; IKAD; Model; A=1-349.
PDB; IKPL; Model; A=1-349.
Genew; HGNC:1603; CCR2.
                                                                                                                                                                                                                                                                                                                                                                                       Name=A;
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                                                                                                                                                                                        Sulfotyrosine.
By similarity.
By similarity.
EFHILAGERIAPLOKPVCGGPGVRPGKNVKVTTGGLLDGR
GKGKGIGRAPBASLQDKEGA -> RYLSVPFRKHITKRFCK
QCPVFYRETVDGVTSTNTPSTGEQEVSAGL (in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR
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16-OCT-2001 (Rel. 40, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
25-OCT-2004 (Rel. 45, Last annotation update)
C-C chemokine receptor type 2 (C-C CKR-2) (CC-CKR-2) (CCR-2)
(Monocyte chemoattractant protein 1 receptor) (MCP-1-R).

Mame-CKR2; Synonyms-CMKBR2;
Macaca mulatta (Rhesus macaque).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDILINE-21354176, PubMed=11461684, DOI=10.1089/088922201750290104,
MEDILINE-21354176, Hauer D.A., Clements J.B.;
Marquiles B.J., Hauer D.A., Clements J.B.;
"Identification and comparison of eleven rhesus macaque chemokine
                                                                                                                                     Cytoplasmic (Potential).
N-linked (GlcNAc. ) (Potential)
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5 (Potential).
(Yopplasmic (Potential).
6 (Potential).
Extracellular (Potential).
7 (Potential).
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V -> I (in dbSNP:1799864).
/FTId=VAR_014339.
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F865E0D39E74CF0F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.
Matches 374; Conservative
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Cytoplasmic (Potential).
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PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G PROTEIN RECEP F1_1; 1.
PROSITE; PS50262; G PROTEIN RECEP F1_2; 1.
G-protein coupled receptor; Transmembrane.
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Interpro; IPR000355; Chmkine_receptor.
Interpro; IPR000276; GPCR_Rhodpsn.
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                                                   301 NPIIYAFVGEKFRYLSMF 319
                                    301 NPIIYAFVGEKFR---SLF
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                                                                                                                                                                                                         Rattus norvegicus (Rat).
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256
277
301
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373
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                                                                                                                                                                                                                                          NCBI_TaxID=10116;
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          AIDS Res. Hum. Retroviruses 17:981-986 (2001).
-!- FUNCTION: Receptor for the MCP-1, MCP-3 and MCP-4 chemokines.
Transduces a signal by increasing the intracellular calcium ions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Gaps
                                                                                                                               ISOId=018793-2; Sequence=Not described;
-!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
Alternative splicing; G-protein coupled receptor; Glycoprotein;
Sulfation; Transmembrane. Extracellular (Potential).
TRANSMEM 43 70 1 (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 (Potential).
Cytoplasmic (Potential).
N-linked (GlCNAc. .) (Potential).
Sulfotyrosine (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1614.5; DB 1; Length 360;
Pred. No. 6.1e-96;
4; Mismatches 4; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                            Cytoplasmic (Potential).
2 (Potential).
Bxtracellular (Potential).
Cytoplasmic (Potential).
4 (Potential).
4 (Potential).
5 (Potential).
5 (Potential).
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Cytoplasmic (Potential).
6 (Potential).
Extracellular (Potential).
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                                                         -!- SUBCELLULAR LOCATION: Integral membrane protein -!- ALTERNATIVE PRODUCTS:
                                                                                 Event=Alternative splicing; Named isoforms=2;
                                                                                                         IsoId=018793-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   similari
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InterPro; IPR000355; Chmkine receptor.
InterPro; IPR000276; GPCR Rhodpsn.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41139 MW;
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Matches 308;
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Jiang Y., Salafranca M.N., Adhikari S., Xia Y., Feng L., Sonntag M.K., deFiebre C.M., Pennell N.A., Streit W.J., Harrison J.K.; "Chemokine receptor expression in cultured glia and rat experimental allergic encephalomyelitis."

J. Neuroimmunol. 86:1-12(18.9);

-I- FUNCTION: Receptor for the MCP-1 (JE), MCP-3 (FIC) and MCP-5 chemokines. Transduces a signal by increasing the intracellular calcium ions level (By similarity).

-I- SUBCELLULAR LOCATION: Integral membrane protein.

-I- TISSUE SPECIFICITY: Expressed in lung, spleen, kidney, thymus and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
25-0CT-2004 (Rel. 45, Last annotation update)
C-C chemokine receptor type 2 (C-C CKR-2) (CC-CKR-2) (CCR2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Sprague-Dawley;
MEDLINE=98318173; PubMed=9655467; DOI=10.1016/S0165-5728(98)00005-8;

    macrophages.
    INDUCTION: In animals in which experimental allergic encephalomyelitis (EAB) has been induced.
    SIMILARITY: Belongs to the G-protein coupled receptor 1 family.

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Potential.
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J. Neurosci. Res. 45:382-391(1996)
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                                                                                                                                                                                                                                                                                       241 AVRVIFTIMIVYFLFWTPYNIVILLINTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
                                                                                                                                                                                                                                                                                                     254 AVRLIFAIMIVYFLFWIPYNIVLFLTTFQEFLGMSNCVVDMHLDQAMQVIETLGMTHCCV 313
                                                                                      9
                                                                                                    Rurihara T., Bravo R.;
"Cloning and functional expression of mCCR2, a murine receptor for the
C-C chemokines UE and FIC.";
J. Biol. Chem. 271:11603-11606 (1996).
                                                                                                                                                                                                                                                     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY
                                                                                                                                                                                      121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK
                                                                                                                                                                                                                                       181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chemoattractant protein 1) and murine macrophage inflammatory protein lalpha receptors: evidence for two closely linked C-C chemokine receptors on chromosome 9.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDINE=97026720; PubMed=8872898; DOI=10.1002/(SICI)1097-4547(19960815)45:4<382::AID-JNR7>3.3.CO;2-H; DOI=10.1002/(SICI)1097-4547(19960815)45:4<382::AID-JNR7>3.3.CO;2-H; Heesen M., Tanabe S., Berman M.A., Yoshizawa I., Luo Y., Kim R., Post T.W., Gerard C., Dorf M.E.; "Mouse astrocytes respond to the chemokines MCP-1 and KC, but reverse transcriptase-polymerase chain reaction does not detect mRNA for the KC or new MCP-1 receptor:"
                                                                                      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN
                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'Molecular cloning and functional expression of murine JE (monocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                     P51683; Q61172;
01-0CT-1996 (Rel. 34, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
25-0CT-2004 (Rel. 45, Last annotation update)
C-C chemokine receptor Lype 2 (C-C CKR-2) (CC-CKR-2) (CCR2)
(JE/FIC receptor) (MCP-1 receptor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-96205938; PubMed-8631787; DOI=10.1074/jbc.271.13.7551;
Boring L., Goaling J., Monteclaro F.S., Lusis A.J., Tsou C.-L.,
Charo I.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=BALB/c;
MEDIINE=96216064; PubMed=8662823; DOI=10.1074/jbc.271.20.11603;
                                                            7;
                                 sery Match 68.4%; Score 1346.5; DB 1; Length 373; st Local Similarity 76.9%; Pred. No. 9.5e-79; tches 257; Conservative 25; Mismatches 45; Indels 7;
126 203 By similarity.
373 AA; 42763 MW; 2E7BB012F5D6FD09 CRC64;
                                                                                                                                                                                                                                                                                                                                        301 NPIIYAFVGEKFR---SLF---HIALG-CRIAPL 327
                                                                                                                                                                                                                                                                                                                                                      373 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=Ccr2; Synonyms=Cmkbr2;
                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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            SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RGO; GO:00164995; F:G-C chemokine receptor activity; IDA.
GO; GO:0019955; F:G-C chemokine receptor activity; IDA.
GO; GO:0019955; F:G-C chemokine response (sensu Vertebrata); IMP.
GO; GO:0016066; P:cellular defense response (sensu Vertebrata); IMP.
GO; GO:00160959; P:hemopoiesis; IMP.
GO; GO:0006959; P:inflammatory response; IMP.
GO; GO:0019233; P:perception of pain; IMP.
RGO; GO:0019334; P:perception of cell migration; IMP.
InterPro; IPR000237; CC_2 receptor.
R InterPro; IPR000255; CMRkine receptor.
R InterPro; IPR000176; GPCR_Rhodpsn.
R Pfam; PR00001; 7tm 1.
R PRINTS; PR000017 Tfm 1.
R PRINTS; PR000017 Tfm 1.
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                 chemokines. Transduces a signal by increasing the intracellular calcium ions level.
--- SUBCELIULAR LOCATION: Integral membrane protein.
--- TISSUE SPECIFICITY: Detected in monocyte/macrophage cell lines, but not in nonhematopoietic cell lines.
--- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
FUNCTION: Receptor for the MCP-1 (JE), MCP-3 (FIC) and MCP-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (Potential).
2 (Potential).
2 (Potential).
Extracellular (Potential).
3 (Potential).
Cytoplasmic (Potential).
4 (Potential).
5 (Potential).
5 (Potential).
Cytoplasmic (Potential).
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es 46; Indels
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184 A -> G (in Ref. 1).

264 V -> G (in Ref. 1).

42782 MW; FA012C10F4C9325A CRC64;
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Extracellular (Potential)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00237; G PROTEIN RECEP F1 1; 1. PROSITE; PS50262; G-PROTEIN RECEP F1 2; 1. G-protein coupled receptor; Transmembrane.
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Y -> H (in Ref
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Cytoplasmic
6 (Potential)
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Matches 255; Conservative
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121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

Zhang Y., Ryder O.A., Zhang Y.;
Zhang Y., Ryder O.A., Zhang Y.;
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.

C. -: SUBCELLULAR LOCATION: Integral membrane protein (By similarity).

C. -: SUBCELLULAR LOCATION: Integral membrane protein (By similarity).

C. -: SUBCELLULAR LOCATION: Integral membrane; IEA.

EMBL, AR177887; AAK43370.1;

C. -: Chemokine receptor activity; IEA.

GO; GO:0016812; F:receptor activity; IEA.

GO; GO:001684; F:rhodopsin-like receptor activity; IEA.

GO; GO:0001864; F:rhodopsin-like receptor protein signalin. ..; IEP

BR GO; GO:0001866; P:G-protein coupled receptor protein signalin. ..; IEP

INTERPRO; IPR0002240; CC 5 receptor.

BR InterPro; IPR000255; Chmkine receptor.

BR InterPro; IPR000255; Chmkine receptor.

BR InterPro; IPR000255; Chmkine receptor.

BR PRINTS; PR00101; 7tm 1, 1.

BR PRINTS; PR01100; CHEWOKINER.

BR RINTS; PR01100; CHEWOKINER.

BR PROSITE; PS01196; COPPER BLUE; UNKNOWN 1.

BR PROSITE; PS01196; COPPER BLUE; UNKNOWN 1.

BR PROSITE; PS01237; GPROTEIN RECEP F1 1, 1.

BR PROSITE; PS0223; G PROTEIN RECEP F1 2, 1.

R G-protein coupled receptor; Receptor; Transmembrane.
                       134 HIGYPGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSGVTWVVAIFASLPGIIFIR
                                                                                                                  4 BVSSPIYDIDYGASBPCQKIDVKQMGAQLLPPLYSMVFLFGFVGNMLVVLILINCKRLKS
                                                                                        181 COKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR
                                                                                                                                                                              AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name-CCR5;
Callicebus moloch (Dusky titi).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Platyrrhini; Cebidae; Callicebinae;
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76.1%; Pred. No. 1e-72;
tive 26; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                         NPIIYAFVGEKFR---SLF---HIALG-CRIAPL 327
                                                                                                                                                                                                                                                                                                    314 NPIIYAFVGEKFRYLSVFFRKHIAKHLCKQCPV 347
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                254 AVRLIPAIMIVYFLFWIPYNIVLFLTTFQESLGMSNCVIDKHLDQAMQVTETLGMTHCCI 313
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                                                                                                         241 AVRVIFTIMIVYFLFWTPYNIVILLNTFOEFFGLSNCESTSOLDOATOVTETLGMTHCCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MLSTSRSRFIRNTNESGEEVTTPPDYDYGAPCHKPDVKQIGAQLLPPLYSLVFIFGFVGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AP006485; BAD08665.1; --
EMBL; AP006485; BAD08655.1; --
EMBL; AP019271; BAD12134.1; --
EMBL; AP019271; BAD12134.1; --
EMBL; AP019271; BAD08655.1; --
EMBL; AP019271; BAD08655.1; --
GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
GO; GO:00018872; F:receptor activity; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:0001586; P:G-protein coupled receptor protein signalin. .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ή.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shinkai H., Morozumi T., Toki D., Eguchi T., Muneta Y., Awata T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shinkai H., Morozumi T., Toki D., Muneta Y., Awata T., Uenishi
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                           05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Chemokine (C-C motif) receptor 2 (Chemokine C-C motif receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Venishi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 67.4%; Score 1327.5; DB 2; Length 373; Best Local Similarity 76.0%; Pred. No. 1.6e-77; Matches 254; Conservative 29; Mismatches 44; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T., Toki D., Muneta Y., Awata T., t
to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SEP-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     373 AA; 42299 MW; FA8E55CA527A34E0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PEAM; PP00001; 7tm_1; 1.
PRINTS; PR00657; CCCHEMOKINER.
PRINTS; PR0107; CHEMOKINER2.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G PROTEIN_RECEP_F1_1; UNKNOWN_1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                            301 NPIIYAFVGEKFR---SLF---HIALG-CRIAPL 327
                                                                                                                                                                                                                                                                                                                                                                  373 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002237; CC 2 receptor.
InterPro; IPR00355; ChmkIne_receptor.
InterPro; IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shinkai H., Morozumi
Submitted (MAY-2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE PROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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Submitted (S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=CCR2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                Q6YT42
                                                                                                                                                                                                                                                                                                                    RESULT 5
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Gaps ; 9

40; Indels

Mismatches

29;

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233; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=CCR5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9TQT3
Matches
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                                                                         243
                                                                                                                                                  311
                                                                                                                                                                                     244 YFLFWAPYNIVLLLNTYQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCVNPIIYAFVGEK 303
                                      184 FGOYRFWKNLETLKAVILGLVLVPLLVAVICYSGILKTLLRCRNEKKRHRAVRLIFTIMLV
RG----WNNFHTIMRNIIGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIV
                                                                                                                                              YPLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Director MGC Project;
Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, BC079752, BAM79756.1;
GO, GO.0004872; Fireceptor activity; IEA.
InterPro; IPR002240; CC 5 receptor.
InterPro; IPR00355; ChmkIne receptor.
InterPro; IPR00355; ChmkIne receptor.
InterPro; IPR00355; GPCR_Rhodpsn.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00196; COPPER BLUE; UNKNOWN 1.
PROSITE; PS00237; G_PROTEIN RECEP_F1_1; UNKNOWN_1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63.3%; Score 1247; DB 2; 75.6%; Pred. No. 2.2e-72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               354 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00001; 7tm 1; 1.
PRINTS; PR0055; CCCHEMOKINER,
TRITES; PR01110; CHEMOKINERS.
PRINTS; PR00237; GPCRRHODOPSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-0CT-2004 (TrEMBLrel. 28, 25-0CT-2004 (TrEMBLrel. 28, 25-0CT-2004 (TrEMBLrel. 28, Chemokine (C-C) receptor 5.
                                                                                                                                                                                                                                                                                                    FRSLF-----HIA 319
                                                                                                                                                                                                                                                                                                                                                                      304 FRNYLLVFFQKHIA 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  354 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=Cmkbr5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Receptor.
SEQUENCE
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                                                                                                                                                  252
                                                                                                                                                                                                                                                                                                 312
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Best Local Similarity

Query Match

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A Kunstwans FROM: N. W. A. Stanton J., Agy M., Shibata R., Yoder A., Fillai S., Kuiken C., Marx P., Wolinksy S.; Submitted (UUL-1999) to the EMBL/GenBank/DDBJ databases.

L. Submitted (UUL-1999) to the EMBL/GenBank/DDBJ databases.

-: SUBCELLULAR LOCATION: Integral membrane protein (By similarity).

-: SIMILARITY: Belongs to family 1 of G-protein coupled receptors. BRBL; AF161935; AAD47691.1; -.

BRBL; AF161935; AAD47691.1; -.

BRBL; AF161936; AAD47691.1; -.

BRBL; AF161939; AAD47691.1; -.

BRBL; AF161940; AAD47691.1; -.

BRBL; AAD4
                                                                                                                 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   310
                                                                                                                                                  194
                                                                                                                                                                                                                                                              125 TIDRYLAIVHAVFAIKARTVNPGVITSVVTWVVAVFVSLDEIIFWRSQKEGSHYTCSPHF 184
                                                                                                                                                                                                                                                                                                                                                                                                       244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              245 VYFLFWTPYNIVLLITTFQEYFGLNNCSSSNRLDQAMQVTETLGMTHCCLNPVIYAFVGE 304
  74
                                                        64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Callithrix jacchus (Common marmoset).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Platyrrhini, Callitrichidae, Callithrix.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 GSIPTYIYDIDYSMSAPCOKFNVKQIAAQLLPPLYSLVFIFGFVGNMMVFLILISCKKLK
                                                                                                                    75 CLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILL
                                                                                                                                                                                                                                   135 TIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYF
                                                                                                                                                                                                                                                                                                                                                                                185 PRIQYRFWKHFQTLKMVILSLILPLLVMVICYSGIINTLFRCRNEKKRHRAVRLIFAIMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                251 VYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGE
17 GEEVITFFDYDY--GAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLK
                                                                                                                                                                                                                                                                                                                                               195 P----RGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
C-C chemokine receptor 5 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        339 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     311 KFRSLFHI 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           305 KFRNYLSV 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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PYNIVILLATFORFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLF- 316
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QGWN98;

QG-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 28, Last annotation update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
CC chemokine receptor 5.

Name=cors;
Callithrix humeralifera (Tassel-eared marmoset).

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WINFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PDYDYG--APCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Soares E.A.J.M., Schrago C.G., Ribeiro I.P., Pissinatti A., Seunez H.N., Russo C.A.M., Tanuri A., Soares M.A.;
"CCR5 chemokine receptor gene evolution in new world monkeys (Platyrrhini, Primates): implication on resistance to lentiviruses."; Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
-i- SUBCELLULAR LOCATION: Integral membrane protein (By similarity)
-i- SIMILARITY: Balongs to family 1 of G-protein coupled receptors.
EMBL; AR161929; AA947661.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0016493; F:c-C chemokine receptor activity; IEA.
GO; GO:0001584; F:raceptor activity; IEA.
GO; GO:0001584; F:raceptor activity; IEA.
GO; GO:0001586; P:raceptor activity; IEA.
GO; GO:0001786; P:raceptor activity; IEA.
       similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63.1%; Score 1244; DB 2; Length 33: 77.3%; Pred. No. 3.3e-72; ive 24; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00196; COPPER BLUE; UNKNOWN 1.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Receptor; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       339 AA; 39164 MW; 6A67CF5D22C70C49
                                                                                                                                                                          InterPro; IPR000923; Bluecu 1.
InterPro; IPR0009240; CC 5 receptor.
InterPro; IPR000240; CC 5 receptor.
InterPro; IPR000355; GmEximaine_receptor.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00627; CGCHRMOKINER.
PRINTS; PR00110; CHEMOKINER.
PRINTS; PR00137; GPCRRHODOPSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 77.3% tes 238; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----HIA 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            303 VFFQKHIA 310
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       183 WKNFETLKWVILGLVLPLLVWVICYSGILKTLIRCRNEKKRHRAVRLIFTIMIVYFLFWA 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 YDIDYGPSEPCRKIDVKQMGAHLLPPLYSMVPLFGFVGNMLVVLILINCKRLKSMTDIYL 62
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SEQUENCE FROM N.A.

MEDLINE=22942991; PubMed=14581567;

DOI=10.1128/JVI.77.22.12310-12318.2003;

BOI=10.1128/JVI.77.22.12310-12318.2003;

Kunstman K.J., Puffer B., Korber B.T., Kuiken C., Smith U.R.,

Kunstman J., Stanton J., Agy M., Shibata R., Yoder A.D., Pillai S.,

Doms R.W., Marx P., Wolinsky S.M.;

"Structure and function of CC-chemokine receptor 5 homologues derived
from representative primate species and subspecies of the taxonomic
suborders Prosimii and Anthropoidea.";

J. Virol. 77:12310-12318(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                     24 FDYDYG--APCHKFDVKQIGAQLLPPLYSLVPIFGFVGNMLVVLILINCKKLKCLTDIYL
                                                                                                                                                                                                                                                                                                                                                                                           12; Gaps
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Platyrrhini; Callitrichidae; Saguinus.
NCBI_TaxID=100754;
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                                                                                                                                                                                                                                                                                                                                            Length 339;
                                                                                                                                                                                                                                                                                                                                                                                         33; Indels
                                                   R PÉGNI PERONOLI TERROLOGIES.

R PÉGNI PPRONOSI TERLI I.

R PRINTS; PRONOSS CCCHEMOKINER.

R PRINTS; PRO1110; CHEMOKINER.

R PRINTS; PRO110; CHEMOKINER.

R PRINTS; PRO110; CHEMOKINER.

R PROSITE; PS00139; CPOPER BLUE; UNKNOWN I.

R PROSITE; PS50262; GPROTEIN RECRE F1 1; I.

R G-procein coupled receptor; Receptor; Transmembrane.

NON TER 319 339

SEQUENCE 339 AA; 39055 MM; C1313952E71B50C7 CRC64:
                                                                                                                                                                                                                                                                                                339 AA; 39055 MW; C1313952E71B50C7 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                          63.1%; Score 1244; DB 2; 76.6%; Pred. No. 3.3e-72; ative 27; Mismatches 33;
  InterPro; IPR002240; CC 5 receptor.
InterPro; IPR000355; Chmkine receptor.
InterPro; IPR000276; GPCR_Rhodpsn.
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Name=CCR5;
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                                            BMBL; AY278744; AAQ2012.1; -
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
GO; GO:0001864; F:rhodopain-like receptor activity; IEA.
GO; GO:0001864; F:rhodopain-like receptor activity; IEA.
InterPro; IPR002249; CC, Freceptor
InterPro; IPR002240; CC, Freceptor.
InterPro; IPR000355; Chmkine_receptor.
InterPro; IPR000365; Chmkine_receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20317091; PubMed=10747879; DOI=10.1074/jbc.M000169200; Mummidi S., Bamshad M., Ahuja S.S., Gonzalez E., Feuillet P.M., Begum K., Galvis M.C., Kostecki V., Valente A.J., Murthy K.K., Haro L., Dolan M.J., Allan J.S., Ahuja S.K., "Evolution of human and non-human primate CC chemokine receptor 5 gene and mRNA. Potential roles for haplotype and mRNA diversity,
                                                                                                                                                                                                                                                                                                                                                                        24 FDYDYG--APCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   198 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT
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Callithixi jacchus (Common marmoset).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix.
                                                                                                                                                                                                                                                                                                                                              Gaps
            similarity)
-1- SIMILARITY: Belongs to family 1 of G-protein (By similarity) EMBL; AV278745; AAQ20013.1; -. EMBL; AV278745; AAQ20013.1; -.
                                                                                                                                                                                                                                                                                                                                              12;
                                                                                                                                                                                                                                                                                                                  63.1%; Score 1244; DB 2; Length 352; 76.6%; Pred. No. 3.4e-72; tive 27; Mismatches 33; Indels 1;
                                                                                                                                                                               PERINTS; PRODOL; 7tm 1; 1.
PRINTS; PRODOS; CCCHEMOKINER.
PRINTS; PRODOS; CCCHEMOKINER.
PRINTS; PRODOS; CHEMOKINER.
PROSITE; PSO0196; COPPER BLUE; UNKNOWN 1.
PROSITE; PSO0237; G PROTEIN RECEP 1; 1; 1.
PROSITE; PSO026; G PROTEIN RECEP 1; 1; 1.
G-protein coupled receptor; Receptor; Transmembrane.
SEQUENCE 352 AA; 40522 MW; FPODOA852E553AF5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
CC chemokine receptor 5 (Chemokine receptor CCR5).
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hes 236; Conservative
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Matches
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Q9MZA0
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RADIENCE FROM N.A.

RADIENCE FROM N.A.

RADIES CAS., Zhang Y.;

Zhang Y., Ryder O.A., Zhang Y.;

Zhang Y., Ryder O.A., Zhang Y.;

Luminted (ang.1999) to the EMBL/GenBank/DDBJ databases.

C. -: SUBCELLULAR LOCATION: Integral membrane protein Coupled receptors.

C. -: SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

C. -: SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

REMBL; AF25264; AAN14530-11; -.

DR EMBL; AF278743; AAQ20011.1; -.

DR EMBL; A7278743; AAQ20011.1; -.

DR EMBL; A7278743; AAQ20011.1; -.

DR EMBL; A7278743; AAQ20011.1; -.

DR GO; GO:0016001; C:integral to membrane; IEA.

GO; GO:001601; C:integral to membrane; IEA.

GO; GO:001601; C:integral to membrane; IEA.

GO; GO:000186; P:C-C chemokine receptor activity; IEA.

GO; GO:000186; P:C-C chemokine receptor activity; IEA.

GO; GO:000186; P:C-C chemokine receptor activity; IEA.

GO; GO:000186; P:C-C chemokine receptor.

InterPro; IPR000254; Bluce.

InterPro; IPR000255; ChmkIne receptor.

InterPro; IPR000255; ChmkIne receptor.

INTERPRO; IPR000276; GPCR Rhodpsn.

PEAN: PR00171; PRM 1.1.

PROSITE; PR00171; GPCRRHODPSN.

DR PROSITE; PR001737; GPCRRHODPSN.

DR PROSITE; PR001737; GPCRRHODPSN.

BRINTS; PR00177; GPCRRHODPSN.

DR PROSITE; PS50262; G-PROTEIN RECEP F1-2; 1.

RPSITE; PRS50262; G-PROTEIN RECEP F1-2; 1.

RPSITE; PR050877; GPCRRHODPSN.

GPCREMONER 352 AA; 40465 MM; FF0D0A8D06F7B8F5 GRC64;
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                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-22174698; Pubmed=12186836;
LaBonte J.A., Babcock G.J., Patel T., Sodroski J.;
LaBockade of HIV-1 infection of New World monkey cells occurs primarily at the stage of virus entry.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Soares E.A.J.M., Schrago C.G., Ribeiro I.P., Pissinatti A., Seuanez H.N., Russo C.A.M., Tanuri A., Soares M.A.; Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
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and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chemoattractant protein 1) and murine macrophage inflammatory protein lalpha receptors: evidence for two closely linked C-C chemokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDDINE-97404635; PubMed-9261347;
Doranz B.J., Lu Z.H., Rucker J., Zhang T.Y., Sharron M., Cen Y.H.,
Wang Z.X., Guo H.H., Du J.G., Accavitti M.A., Doms R.W., Peiper S.C.;
"Two distinct CCR5 domains can mediate coreceptor usage by human
                             CKRS MOUSE STANDARD; PRT; 354 AA.
P51682; 035313; 035891; P97308; P97405; Q61867;
01-0CT-1996 (Rel. 34, Created)
15-UTL-1998 (Rel. 36, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (MIP-1
                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=129/SvJ; TISSUE=Spleen;
MEDLINE=96205938; PubMed=8631787; DOI=10.1074/jbc.271.13.7551;
MEDLINE=96205938; PubMed=8631787; DOI=10.1074/jbc.271.13.7551;
MEDLINE=96205938; PubMed=8631787; DOI=10.1074/jbc.271.13.7551;
Charo I.F.;
"Molecular cloning and functional expression of murine JB (monocyte)"
                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=C57BL/6, and NIH Swiss; TISSUE=Kidney, Liver, and Spleen; MEDLINE=98001387; PubMed=934322; Kozak S.L., Kabat D.; Platt B.J., Kozak S.L., Kabat D.; In the CCR5 genes of African green monkeys and mice implicate specific amino acids in infections by simian and human immunodeficiency viruses.";
                                                                                                                                                                                                                                                                                                              MEDLINE=9677810; PubMed=866280; DOI=10.1074/jbc.271.24.14445; Meyer A., Coyle A.J., Proudfoot A.E.I., Wells T.N.C., Power C.A.; Cloning and characterization of a novel murine macrophage inflammatory protein-1 alpha receptor."; Biol. Chem. 271:14445-14451(1996).
                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                      Kuziel W.A., Beck M.A., Dawson T.C., Maeda N.;
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                        STRAIN=C57BL/6 X CBA; TISSUE=Thymus;
                                                                                                                                                                                                                                                                      Biol. Chem. 271:7551-7558(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immunodeficiency virus type 1.";
J. Virol. 71:6305-6314(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Virol. 71:8642-8656(1997).
                                                                                                                                                                                                                                                             receptors on chromosome 9.";
                                                                                                        Name=Ccr5; Synonyms=Cmkbr5;
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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(See http://www.isb-sib.ch/announce/
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PRINTS; PR00021; 7Em 1: 1.

PROSITE; PS00237; GFCRHODDFN.

PROSITE; PS50262; GFROTEIN RECEP F1 1; 1.

PROSITE; PS50262; GFROTEIN RECEP F1 2; 1.

PROSITE: PS50262; GFROTEIN RECEP F1 1; 1.

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PS50262; GFROTEIN RECEP F1 1; 1.

PS50262; GFROTEIN RECEP F1 1; 1.

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                                                     entities requires a license agreement (St
or send an email to license@isb-sib.ch).
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24. Zhang Y., Ryder O.A., Zhang Y.;

25. Zhang Y., Ryder O.A., Zhang Y.;

26. Zhang Y., Ryder O.A., Zhang Y.;

27. Submitted (AUC1999) to the EMBL/GenBank/DDBJ databases.

28. STATIONS INTEGERAL membrane protein (By similarity).

29. STATIONS INTEGERAL MEMBRITY: Belongs to family 1 of G-protein coupled receptors.

20. STATIONS INTEGERAL CONTRESS OF A STATIONS INTEGERAL.

20. GO:0016493; F:C-C chemokine receptor activity; IEA.

20. GO:0016493; F:C-C chemokine receptor activity; IEA.

20. GO:000186; F:Receptor activity; IEA.

30. GO:000186; F:Receptor activity; IEA.

31. STATION INTEGERAL CONTRESS OF A STATION 
                                                                                                                                                                                                         123 IVHAVFALKARTVTFGVVTSVITWLVAVFASLPGIIFTRSQKEGYHYTCSPHYPFGQYQF
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24 FDYDYG--APCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIYL
                                                  3 YDIDYGPSEPCRKIDVKQMGAHLLPPLYSMVFLFGFVGNMLVVLILINCKRPKSMTDIYL
                                                                                                                                                               82 INLAISDLIFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLA
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Platyrrhini, Cebidae, Atelinae, Ateles.
NCBI_TaxID=9509;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DAR-2004 (TrEMBLrel. 26, Last annotation update)
C-C chemokine receptor 5.
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Best Local Similarity 76.64
Matches 236; Conservative
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Q95NC4;
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                                                                                                                                                                                                         245 VYFLFWTPXNIVLLITTFQEFFGLNNCSSSNRLDQAMQATETLGMTHCCLNPVIYAFVGE 304
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EMBL; AF161926; AAD47683.1; --
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
GO; GO:0016849; F:rhodopsin-like receptor activity; IEA.
GO; GO:0001886; F:rhodopsin-like receptor activity; IEA.
GO; GO:0001886; F:rhodopsin-like receptor protein signalin. . .; IEA.
InterPro; IPR0002249; CC 5 receptor.
InterPro; IPR000355; Chmkine receptor.
InterPro; IPR000276; GPCR_Rhodopsn.
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DOI=10.1128/JVI.77.22.12310-12318.2003;
Kunstman K.J., Puffer B., Korber B.T., Kuiken C., Smith U.R.,
Kunstman J., Stanton J., Agy M., Shibata R., Yoder A.D., Pillai S.,
Doms R.W., Marx P., Wolinsky S.M.;
"Structure and function of CC-chemokine receptor 5 homologues derived
from representative primate species and subspecies of the taxonomic
suborders Prosimii and Anthropoidea.";
J. Virol. 77:12310-12318(2003).
    PRG----wnnfhtimrnilglulpllimvicysgilktilrcrnekkrhraurviftimi
                                                  185 PHTOYHFWKSFQTLKMVILSLILPLLVMIICYSGILHTLFRCRNEKKRHRAVRLIFAIMI
                                                                                                                                                                   251 VYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.;
Submitted (JUL.1993) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
EMBL, AF161925; AAD47682.1; -.
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Mammalia, Eutheria, Primates, Platyrrhini, Callitrichidae, Saguinus,
NCBI_TaxID=100754;
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PRINTS; PR01110; CHEMOKINERS.
PRINTS; PR01210; CHEMOKINERS.
PROSITE; PS00124; GPCRRHODOPSN.
PROSITE; PS00237; GPROTEIN RECEP F1 1; 1.
PROSITE; PS50262; GPROTEIN_RECEP_F1 2; 1.
G-protein coupled receptor; Receptor; Transmembrane.
NON_TER 339 339
SEQUENCE 339 AA; 39081 MW; 6B79D05D22C70032 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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Matches 237; Conserv
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190 WKNPEALKOVILGLVLPLLVAVICYSGILKTILRCRNEKKRHRAVRLIFTIMIVYFLFWA 249
                                                                           WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT
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                                                                  WNNPHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 257
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                                        LNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLA
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                                                                                                                                                                                                                                                                         Leontopithecus chrysopygus (Gold-and-black lion tamarin).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi,
Mammalia, Eutheria, Primates, Platyrrhini, Callitrichidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 63.0%; Score 1241; DB 2; Length 352; Best Local Similarity 76.3%; Pred. No. 5.3e-72; Matches 235; Conservative 27; Mismatches 34; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PRO0657; CCCHEMOKINER.
PRINTS; PRO1110; CHEMOKINERS.
PRINTS; PRO0137; GCRRHODOPSN.
PROSITE; PS00196; COPPER BLUB; UNKNOWN 1.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS00262; G PROTEIN RECEP F1 2; 1.
G-proctein coupled receptor; Receptor; Transmembrane.
SEQUENCE 352 AA; 40437 MW; 5EC1884238503783 CRC64;
                                                                                                                                                                                                                            05-JUL_2004 (TrEMBLrel. 27, Created)
05-JUL_2004 (TrEMBLrel. 27, Last sequence update)
05-JUL_2004 (TrEMBLrel. 27, Last annotation update)
CC chemokine receptor 5.
                                                                                                                                                                                                            352 AA.
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                                                                                                                                                              310 VFFQKHIA 317
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NCBI_TaxID=58710;
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US-09-195-662A-2

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Copyright (c) 1993 - 2005 Compugen Ltd.
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PCT-US95-00476-2
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US-09-131-827A-20
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Maximum DB seq length: 2000000000
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RESULT 1

US-08-450-333A-2

US-08-450-333A-2

Sequence 2, Application US/0845033A

Parent No. 5707015.

GENERAL INFORMATION:

JILL OR INVENTION: PARMALLAN MONOCITE GIBMOATTRACTANT

TITLE OF INVENTION: PARMALLAN MONOCITE GIBMOATTRACTANT

TITLE OF INVENTION: PROFILE SECTION PROFILE SECTI
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61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
                                                                                                                                                       1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
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Best Local Similarity 100.
Matches 374; Conservative
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ORGANISM: Homo sapiens
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                           61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No. 6132987;
GENERAL INFORMATION:
APPLICANT: Charo, Israel
APPLICANT: COURLIN, Shaun
TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT;
TITLE OF INVENTION: PROTEIN RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
STREET: 5 Palo Alto
CITY: Palo Alto
STATE: California
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ZIP: 94306-2155

COMPUTER READABLE FORM:
MEDIUW TYPE: FIDOPPY disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,669
FILING DATE: May 25, 1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
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100 0%; Score 1970; DB 3;
Best Local Similarity 1100.0%; Pred. No. 4.3e-150;
Matches 374; Conservative 0; Mismatches 0;
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REGISTRATION NUMBER: 30,092
REFERENCE/DOCKET NUMBER: UCAL-237/01US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-843-5000
TELEFAX: 415-857-0663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08446669
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amino acid
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TELEX: 380816CooleyPA
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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JOS-10-10-103-1034-1034-104

j Gequence 14, Application US/10039659A

j Patent No. 672350.

GENERAL INFORMATION:

APPLICANT: Gish, Kurt C.

APPLICANT: Gish, Kurt C.

APPLICANT: Schall, Thomas J.

APPLICANT: Schall, Alain P.

APPLICANT: Jointk, Albert

TITLE OF INTERTION: Antibodies that bind chemokine TECK

FILE REPERENCE: DXOS89XIB US/10/039,659A

CURRENT PILING DATE: 2002-01-03

PRIOR APPLICATION NUMBER: US 08/887,977

PRIOR PILING DATE: 1997-07-03

PRIOR PILING DATE: 1996-07-05

NUMBER OF SEQ ID NOS: 26

NUMBER OF SEQ ID NOS: 26

SOFTHARE: PATENTIN VERSION 3.1
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HIGYEGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
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61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLFLWAHSAANEWVFGNAMCKLFTGLY 120
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GENERAL INFORMATION:
APPLICANT: THE REGENTS OF the University of California TITLE OF INVENTION:
MANMALIAN MONOCYTE CHEMOATTRACTANT TITLE OF INVENTION: PROTEIN RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Robbins, Berliner & Carson STREET: 201 N. Figueroa Street, 5th Floor CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Berliner, Robert
REGISTRATION NUMBER: 20,121
REFERENCE/DOCKET NUMBER: 5555
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-977-1001
                                                                                                                                                                                                                                                                                                                                                                                                                    GRAPEASLQDKEGA 374
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amino acid
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                     181 CQXEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
STREET: 5 Palo Alto Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANI: CHEALU, Shaun
Coughlin, Shaun
TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
PROTEIN RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94306-2155
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: UCAL-237/01US TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/446,669
FILING DATE: May 25, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/625,573
FILING DATE: 25-JUJ-2000
CLASSIFICATION: <Unknown>
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Neeley, Richard
REGISTRATION NUMBER: 30,092
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/09625573
Patent No. 6730301
GENERAL INFORMATION:
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STATE: California
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us-10-791-166-2.rai

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61 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID 120
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78 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID 137
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                                                                                                                                                                                                                                                                                                                  POLYNUCLEOTIDES ENCODING HUMAN G-PROTEIN
CHEMOKINE RECEPTOR HDGNR10 (AS AMENDED)
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Pred. No. 2.3e-138;
                                                                                                                                                                                                                                                                                                                                                                                           SSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C. F: 1100 NEW YORK AVE., NW, SUITE 600 WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: REALBLE FORD

COMPUTER: IN PC Compatible

COMPUTER: IN PC Compatible

COMPATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,343D

FILING DATE: 06-UN-1995

CLASSIFTCATION: 435

ATYONEY/AGENT INPORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688

REFERENCE/DOCKET NUMBER: 1488.1150000/EKS/KLM

TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION STOLES:
SEQUENCE CHARACTERISTICS:
INPORMATION FOR SEQ 1D NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 92.5%; Score 1823; D
Best Local Similarity 100.0%; Pred. No. 2.3
Matches 344; Conservative 0; Mismatches
                                                                                                                                                                                                                     Sequence 9, Application US/08466343D
Fatent No. 6025154
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDS
                                                                     361 GRAPEASLODKEGA 374
                                                                                                              374 GRAPEASLODKEGA 387
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TYPE: amino acid
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TOPOLOGY: linear
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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US-08-466-343D-9
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE REPERBENGE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT PILING DATE: 2000-04-14
PRIOR PELICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOUTHANDER OF SEQ ID NOS: 207012
SOUTHANDER PASSES FOR Windows Version 4.0
SEQ ID NO 11222
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                                                  HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
      61 MLVVLILINCKKCKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 11222, Application US/09949016 Patent No. 6812339
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converse of Application US/09339912A

patent No. 675919

GENERAL INFORMATION:

APPLICANT: Li, Yi

APPLICANT: Li, Xi

TITLE OF INVENTION: Antibodies to Human G-Protein Chemokine Receptor HDGNR10

TITLE OF INVENTION: (CCRS Receptor)

TITLE OF INVENTION: ANTibodies to Human G-Protein Chemokine Receptor HDGNR10

TITLE OF INVENTION: (CCRS Receptor)

TITLE OF INVENTION: (CCRS Receptor)

TITLE OF INVENTION: ANTIBOR: 1999-06-25

PRIOR APPLICATION NUMBER: 1999-06-25

PRIOR PELING DATE: 1998-11-18

PRIOR APPLICATION NUMBER: 09/195,662

PRIOR PRIOR OATE: 1998-11-18

PRIOR PRIOR OATE: 1998-11-18

PRIOR PRIOR PLILING DATE: 1998-10-06

NUMBER OF SEQ ID NOS: 9

SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                     78 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    166 WANPHIIMRANILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          226 PYNIVILLANTPQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPITYAFVGEKFRSLFH 285
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                                                                                                                                                                                                                                                                               1 BEVITFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLLLINCKKLKCLT 60
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                                                                                                                                                                             DB 4; Length 329;
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                                                                                                                                                                          Score 1727.5; DB 4
Pred. No. 9.8e-131;
                                                                                                                                                                                                                             0; Mismatches
SOFTWARE: PatentIn version 3.0 SEQ ID NO 9 LEGITH: 329 TYPE: PRT
                                                                                                                                                                          Query Match
Best Local Similarity 95.6%;
Matches 329; Conservative
                                                                                             ; ORGANISM: Protein
US-09-502-783A-9
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US-09-339-912A-9
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US-09-339-912A-9
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Patent No. 6511826
GENERAL INPORMATION:
APPLICANT: Li, Yi
APPLICANT: Li, Yi
TITLE OF INVENTION: POLYMUCIECTIDES Encoding Human G-Protein Chemokine Receptor (CCRS)
TITLE OF INVENTION: HDGNIO
FILE REPRENCE: 1488.1150006
CURRENT APPLICATION NUMBER: US/09/502,783A
CURRENT FILING DATE: 2001-08-23
PRIOR APPLICATION NUMBER: 08/466,343
PRIOR FILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 9
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                                                                                                                                                                                                                                             APPLICANT: Li, Yi
APPLICANT: Li, Yi
APPLICANT: Li, Yi
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Methods of Screening Using Human G-Protein
TITLE OF INVENTION: Chemokine Receptor HDGNRIO (CCR5)
TITLE OF INVENTION: Chemokine Receptor HDGNRIO (CCR5)
FILE REPERRINGE: 1488.1150005
CURRENT FILING DATE: 1090-02-11
PRIOR PELLING DATE: 1998-11-18
PRIOR PELLING DATE: 1998-11-18
PRIOR FILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Version 3.1
SEQ ID NO 9
LENGTH: 344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 344;
     318 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 361
                                  301 IALGCRIAPLOKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 92.5%; Score 1823; DB 4; Length 3 Best Local Similarity 100.0%; Pred. No. 2.3e-138; Matches 344; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                          Sequence 9, Application US/09502784A Patent No. 6743594 GENERAL INFORMATION:
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US-09-502-784A-9
                                                                                                                               RESULT 8
US-09-502-784A-9
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US-09-502-783A-9
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TOPOLOGY:
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US-08-446-669-4
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APPLICANT: Li, Yi
APPLICANT: Li, Yi
APPLICANT: Ruben, Steven, M.
TITLE OF INVENTION: Human G-Protein Chemokine Receptor HDGNR10 (CCR5 Receptor)
FILE REPERENCE: 1488.1150002
CURRENT APPLICATION NUMBER: US/09/195,662A
CURRENT FILING DATE: 1998-11-18
PRIOR APPLICATION NUMBER: 094466,343
PRIOR FILING DATE: 1995-06-06
NUMBER: Patentin version 3.0
SEQ ID NO 9
LENGTH: 329
                                                                                                                                                      258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 317
                                                                                                                                                                                    226 PYNIVILLINTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 285
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                                                                   198 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 257
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87.7%; Score 1727.5; DB 4; Length 329;
Best Local Similarity 95.6%; Pred. No. 9.8e-131;
Matches 329; Conservative 0; Mismatches 0; Indels 15;
                                                                                                                                                                                                                                          318 IALGCRIAPLOKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 361
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APPLICANT: Charc, Israel
APPLICANT: Coughlin, Shaun
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 9, Application US/09195662A Patent No. 6800729
                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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ORGANISM: Protein
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US-08-450-393A-4
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241 AVRVIFTIMIVYFLFWTPYNIVILLMTFQEFFGLSNCESTSQLDQATQVTETLGWTHCCI 300
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Patent No. 6132987
GENERAL INFORMATION:
APPLICANT: Charo, Israel
APPLICANT: Coughlin, Shaun
TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
TITLE OF INVENTION: PROTEIN RECEPTORS
MAMMALIAN MONOCYTE CHEMOATTRACTANT PROTEIN RECEPTORS
                                                                                                                                           CITY: Palo Alto
COUNTRY: USA
CONFUTER: California
CONFUTER: California
COMPUTER READABLE FORM:
MEDIUM TYPE: Bloppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOUTWARE: Parentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/450,393A
FILING DATE: May 25, 1995
CLASSIFICATION: 424
ATTORNEY/ACENT INFORMATION:
NAME: CSerr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: UCAL-237/02US
TELEFOOMMUNICATION INFORMATION:
TELEFOOMMUNICATION INFORMATION:
TELEFAX: 380816CooleyPA
INFORMATION FOR SEQ ID NO: 4:
INFORMATION FOR SEQ ID NO: 4:
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Pred. No. 1.3e-124;
3; Mismatches 5;
                                                                                                    Cooley Godward Castro Huddleson &
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TITLE OF INVENTION: MAMMALIAN ITILE OF INVENTION: PROTEIN RE NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSE: Cooley Godward Ca STREET: 5 Palo Alto Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 95.5%;
Matches 319; Conservative
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TYPE: amino acid
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CEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/045,583
FILING DATE: 20-MR-98
CLASSIPICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
ATTORNEY.**
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCS/DOCKET NUMBER: MNI-044
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Therefor
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TELEFAX: (617)742-4214
INPORMATION POR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 amino acids
TYPE: amino acids
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Best Local Similarity 95.5%;
Matches 319; Conservative
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                     Massachusetts
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Patent No. 6287805
GENERAL INFORMATION:
APPLICANT: Graham, Gerard J. et al.
TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESSE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQ1CAQLLPPLYSLVF1FGFVGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 3; Length 360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
           CORRESPONDENCE ADDRESS:
ADDRESSER: Cooley Godward Castro Huddleson & Tatum STREET: 5 Palo Alto Square
STRY: Palo Alto
STATE: California
                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,669
FILING DATE: MAY 25, 1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1651.5; DB Pred. No. 1.3e-124 3; Mismatches 5
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                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Neeley, Richard
REGISTRATION NUMBER: 30,092
REFERENCE/DOCKET NUMBER: UCAL-
TELEPONE: 415-849-500
TELEPAX: 415-857-663
TELEX: 308016CooleyPA
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 95.5%;
Matches 319; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                360 amino acids
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NUMBER OF SEQUENCES:
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                                                                                                           USA
                                                                                        STATE: C.
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TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled
Heptahelical Receptor Superfamily and Uses
                                                                                                                                       1 MLSTSRSRFIRNTNESGEEVTTFPDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN
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                                                                       Gaps
                                                                       7;
   Length 360;
   DB 3;
Score 1651.5; DB 3
Pred. No. 1.3e-124;
3; Mismatches 5;
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ADDRESSEE: LAHIVE & COCKFIELD, LLP
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                                                                                                           COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/534,185

FILING DATE: 24-Mar-2000

CLASSIFICATION NUMBER: 09/045,583

FILING DATE: CURROWN-

PRIOR APPLICATION NUMBER: 09/045,583

FILING DATE: CURROWN-

ATTORNEY/AGENT INFORMATION:

NAME: Mandragouras, Amy E.

REGISTRATION NUMBER: 34,207

REGISTRATION NUMBER: MAI-044

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION FOR SEQ ID NO: 50:

SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: peptide

FRAGMENT TYPE: internal

SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-09-534-185-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 360 amino acide TYPE: amino acid
STREET: 28 State Street
                             CITY: Boston
STATE: Massachusetts
COUNTRY: USA
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Search completed: June 9, 2005, 16:50:10 Job time: 32.0817 secs

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June 9, 2005, 16:48:19; Search time 104.455 Seconds (without alignments) 1372.524 Million cell updates/sec
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1970
1 MLSTSRSRFIRNTNESGEEV.....GKGKSIGRAPEASLQDKEGA 374
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                             OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		,			SUMMARIES		
Segult		مه درو					
No.	Score	Match	Match Length DB	DB	ID	Description	
	1970	100.0		ដ	US-09-893-512-13	Sequence 13, Appl	
7	1970	100.0	374	14	US-10-039-659-14	Sequence 14, Appl	
m	1970	100.0		14	US-10-239-423-63	Sequence 63, Appl	
4	1970	100.0		16	US-10-754-071-14	Sequence 14, Appl	
Ŋ	1970	100.0		16	US-10-741-601-287	Sequence 287, App	
9	1970	100.0		16	US-10-791-592-2	Sequence 2, Appli	
7	1970	100.0		16	US-10-791-166-2	Sequence 2, Appli	
60	1970	100.0		11	US-10-759-860-14	Sequence 14, Appl	
Q	1970	100.0		17	US-10-799-736-13	Sequence 13, Appl	
10	1823	92.5		9	US-09-779-879A-9	Sequence 9, Appli	
11	1823	92.5		6	US-09-779-880A-9	Sequence 9, Appli	

Sequence 9, Appli Sequence 9, Appli Sequence 9, Appli	0,0	0,0	Sequence 9, Appli	,	460,	20,	64,	8,	28	e 28(e 4,	4,	ø	4	8	20,	7,	7,	7, A	Sequence 473, App	7,	۲,	4	51,	'n	Sequence 3, Appli	Sequence 3, Appli	Ä	Ä
.4 US-10-232-686-9 .4 US-10-067-800-9 .4 US-10-135-839-9	9 US-09-725-285-9 9 US-09-195-662A-9	US-09-339-912A-9) US-09-502-783A-9 6 HS-10-791-905-9	US-09-131-827A-2	.4 US-10-225-567A-460	.4 US-10-164-649-50	10-239-423	US-10	10-741-601-28	US-10		US-10	.6 US-10-700-313-8		.7 US-10-846-185-8	US-09-131-827A-20	US-09-938-719-7	US-09-939-226-7	US-09-938-703-7	US-09-826-509	.6 US-10-661-798-7			4 US-10-164-64	9 US-09-104-792-3	US-10	US-10-893	.0 US-09-893-512-14	7 US-10-799-736-14
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1823 1823 1823	1727.5	1727.5	1727.5	1651.5	1651.5	1651.5	1651.5	1651.5	1651.5	1651.5	1651.5	1651.5	1651.5	1651.5	1651.5	1650.5	1645.5	1645.5	1645.5	1645.5	1645.5	1645.5	1645.5	•	1589.5	1589.5	1589.5	1582.5	1582.5
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ALIGNMENTS

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61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

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TITLE OF INVENTION: Diagnostic Agent and Medicament for Examining the TITLE OF INVENTION: Diagnostic Agent and Medicament for Examining the TITLE OF INVENTION: Cell Surface Proteome of Tumor and Inflammation Cells and TITLE OF INVENTION: Freferably with the Aid of Specific Chemokine TITLE OF INVENTION: Preferably with the Aid of Specific Chemokine TITLE OF INVENTION: Receptor Analysis and Chemokine Receptor/Ligand Interaction FILE REFERENCE: 022217us
CURRENT PELING DATE: 2020-09-23
PRIOR PAPLICATION NUMBER: DELOGIGO13.1
PRIOR FILING DATE: 2000-09-31
NUMBER OF SEQ ID NOS: 84
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 63
LENGTH: 374
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                                                                                                                                                                                                                                                                                                                                                                                                                           121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVPASVPGIIFTK
                                                                                                                                                                               1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN
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                                                                           Length 374;
                                                                                                                                 Indels
                                                                           Score 1970; DB 14;
Pred. No. 3.4e-163;
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                                                                                                                                 0; Mismatches
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
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Publication No. US20030186889A1
GENERAL INFORMATION:
                                                                              100.0%;
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ORGANISM: Artificial Sequence
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Matches 374; Conservative
                                                                                                      Best Local Similarity 100.
Matches 374; Conservative
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US-10-039-659-14
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                          61 MLVVLILINCKKLKCLTDIYLLMLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
                                                                                                                                                                                                                                       181 COKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNBKKRHR
                                                                                                                                                                                       CQKEDSVYVCGPYPPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR
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                                                                                                                                                                                                                                                                                                                                                                                                 301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI
  COMPUTER READMELE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/039,659
FILING DATE: 03-Jan-2002
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 60/021,644
FILING DATE: 05-JUL-1997
APPLICATION NUMBER: US 60/021,644
FILING DATE: 11-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schall, Thomas J.
Schall, Alain P.
Zlotnik, Albert
TITLE OF INVENTION: MAMMALIAN CHEMOKINE REAGENTS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: DNAX Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0589K1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
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TELEPHONE: 650-652-9192
TELEFAX: 650-496-1200
RMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 14, Application US/10039659
Publication No. US20030018167A1
GENERAL INFORMATION:
APPLICANT: Wang, Wei
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US-10-039-659-14
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Db 181 CQKEDSVYVCGPYPPRGMNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR Cy 241 AVRVIFTIMIVYPLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGWTHCCI	RESULT 5 US-10-741-601-287 is Sequence 287, Application US/10741601 is Sequence 287, Application US/10741601 is Publication No. US20040166519A1 is GENERAL INFORMATION: is APPLICANT: CARGILL, Michele et al. is TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF is TILE REPERENCE: CLOOLSOO is CURRENT APPLICATION NUMBER: US/10/741,601 is CURRENT FILING DATE: 2003-12-22 is NOFTWARE: FastSEQ for Windows Version 4.0 is SEQ ID NO 287 is LENGTH: 374 is TYPE: PRT is ORGANISM: Homo sapiens US-10-741-601-287	Query Match 100.0%; Score 1970; DB 16; Length 374; Best Local Similarity 100.0%; Pred. No. 3.4e-163; Accessive 100.0%; Pred. No. 3.4e-163; Qy 1 MLSTSRSRFIRNTNESGEEVTTFPDYDYGAPCHKPDVKQIGAQLIPPLYSLVFIFGFVGN Qy INLSTSRSRFIRNTNESGEEVTTFPDYDYGAPCHKPDVKQIGAQLIPPLYSLVFIFGFVGN Qy 61 MLVVLILLINCKKLKCLTDIYLLNIAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY Db 61 MLVVLILLINCKKLKCLTDIYLLNIAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY Qy 121 HIGYFGGIFFIILLTIDRYLAINTANYALKARTVTFGVVTSVITMLVAVFASVPGIIFTK Db 121 HIGYFGGIFFIILLTIDRYLAINTANYALKARTVTFGVVTSVITMLVAVFASVPGIIFTK Db 121 HIGYFGGIFFIILLTIDRYLAINTANYALKARTVTFGVVTSVITMLVAVFASVPGIIFTK Db 121 HIGYFGGIFFIILLTIDRYLAINTANYALKARTVTFGVVTSVITMLVAVFASVPGIIFTK	QY 181 COKEDSUYVCGPYPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR Db 181 COKEDSUYVCGPYPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR QY 241 AVRVIFTIMIVYFLFWTPYNIVILLATFQBFFGLSNCESTSQLDQATQVTETLGMTHCCI Db 241 AVRVIFTIMIVYFLFWTPYNIVILLATFQBFFGLSNCESTSQLDQATQVTETLGMTHCCI Db 301 NPIIYAFVGEKFRSLFHTALGCRIAPLQKFVCGGPGVRPGKNVKYTTQGLLDGRGKGKSI Db 301 NPIIYAFVGEKFRSLFHTALGCRIAPLQKFVCGGPGVRPGKNVKYTTQGLLDGRGKGKSI QY 361 GRAPEASLQDKEGA 374 Db 361 GRAPEASLQDKEGA 374	RESULT 6 US-10-791-592-2 ; Sequence 2, Application US/10791592 ; Publication No. US20040219644A1
61 MLVVLILINCKGLKCLTDIYLLANISDLLFLTLFLWAHSAANEWVFGNAMCKLFTGLY 120 121 HIGYFGGIPPIILLTIDRYLAYHAVBALKAFTVTFGVYTSVITWLVAVFASVPGIIFTK 180 121 HIGYFGGIPFIILLTIDRYLAYHAVBALKAFTVTFGVYTSVITWLVAVFASVPGIIFTK 180 121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKAFTITHITHITHITHITHITHITHITHITHITHITHITHITH	301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKEVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360	FILE REFERENCE: DXOSGSYLC US CURRENT APPLICATION NUMBER: US/10/754,071 CURRENT APPLICATION NUMBER: US/10/754,071 FILING DATE: 2004-01-07 PRIOR APPLICATION NUMBER: US 10/039,659 PRIOR FILING DATE: 2002-01-03 PRIOR FILING DATE: 1997-07-03 PRIOR FILING DATE: 1997-07-05 PRIOR FILING DATE: 1996-07-05 PRIOR FILING DATE: 1996-07-05 PRIOR FILING DATE: 1996-10-11 PRIOR FILING DATE: 1997-06-04 NUMBER: 1997-06-04		121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

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361 GRAPEASLQDKEGA 374
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Matches 374; Conservative
                                                            RESULT 7
US-10-791-166-2
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                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
STREET: 5 Palo Alto Square
                 Coughlin, Shaun
TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNBER: US/10/791,592
FILING DATE: 01-Mar-2004
CLASSIFICATION: <UNknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Neeley, Richard
REGISTRATION NUMBER: 30,092
REFERENCE/DOCKET NUMBER: UCAL-237/01US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/625,573
FILING DATE: 25-Jul-2000
APPLICATION NUMBER: US/08/446,669
FILING DATE: May 25, 1995
ATTORNEY/AGENT INFORMATION:
                                                          PROTEIN RECEPTORS
                                                                                                                                                                                                                       ZIP: 94306-Z155
COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear; MOLECULE TYPE: protein; SEQUENCE DESCRIPTION: SEQ ID NO: 2: US-10-791-592-2
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TYPE: amino acid
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                                                                                 NUMBER OF SEQUENCES: 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 2
                                                                                                                                                               CITY: Palo Alto
STATE: California
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Matches 374; Conservative
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                                                                                                                                                                         NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
STREET: 5 Palo Alto Square
CITY: Palo Alto
STATE: California
COUNTRY: USA
                                                                                                Coughlin, Shaun
TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC_Compatible
COMPUTER: IBM PC_COMPATIBLE
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/10/791,166
FILING DATE: 01-Mar-2004
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Neeley, Richard
REGISTRATION NUMBER: 30,092
REFERENCE/DOCKET NUMBER: UCAL-237/01US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-843-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/625,573
FILING DATE: 25-Jul-2000
APPLICATION NUMBER: US/08/446,669
                                                                                                                                                    PROTEIN RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: May 25, 1995
                                                                                                                                                                                                                                                                                                                                                ZIP: 94306-2155
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
Sequence 2, Application US/10791166
Publication No. US20040223968A1
GENERAL INFORMATION:
APPLICANT: Charo, Israel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 374 amino acids
TYPE: amino acid
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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61 MLVVLILINCKKLKCLTDIYLLINLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
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                                                                                  US-10-799-736-13

US-10-799-736-13

US-10-799-736-13

Sequence 13, Application US/10799736

Publication No. US20050118675A1

GENERAL INFORMATION:

APPLICANT: OWNAN, CHRISTER

TITLE OF INVENTION: RECEPTOR

TITLE OF INVENTION: RECEPTOR

FILE REFERENCE: 07675-0001-03 SEQUENCE LISTING

CURRENT APPLICATION NUMBER: US/09/993,512

PRIOR PILIATION NUMBER: US/09/993,512

PRIOR FILING DATE: 1999-10-14

PRIOR FILING DATE: 1999-10-14

PRIOR PILING DATE: 1999-10-14

PRIOR PILING DATE: 1999-10-14

PRIOR PILING DATE: 1999-10-14

PRIOR PILING DATE: 1999-10-13

NUMBER OF SEQ ID NOS: 16

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 13
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Patent No. US20020048786A1
GENERAL INFORMATION:
APPLICANT: Rosen, Craig A.
APPLICANT: Rosechke, Viktor
APPLICANT: Ruben, Steven, M.
TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10
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     361 GRAPEASLQDKEGA 374
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US-10-799-736-13
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                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Gish, Kurt C.
APPLICANT: Gish, Kurt C.
APPLICANT: Gish, Kurt C.
APPLICANT: Schall, Thomas J.
APPLICANT: Schall, Thomas J.
APPLICANT: Zlotnik, Alain P.
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: Methods for using chemokine TECK
FILE REFERENCE: DX589KID US
CURRENT APPLICATION NUMBER: US/10/759,860
CURRENT FILING DATE: 2004-01-16
PRIOR FILING DATE: 1997-07-03
PRIOR FILING DATE: 1997-07-03
PRIOR FILING DATE: 1996-07-05
PRIOR FILING DATE: 1996-07-05
PRIOR FILING DATE: 1996-07-05
PRIOR FILING DATE: 1997-06-04
PRIOR FILING DATE: 1997-06-04
PRIOR FILING DATE: 1997-06-04
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.1
SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                            Sequence 14, Application US/10759860 Publication No. US20050074790A1 GENERAL INFORMATION:
                                                                                                                                                       361 GRAPEASLQDKEGA 374
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Best Local Similarity 100.
Matches 374; Conservative
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US-10-759-860-14
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Faquence 9, Application US/09779880A

Facent No. US20020061834A1

GENERAL INFORMATION:

APPLICANT: Rosen, Craig A.

APPLICANT: Rosen, Viktor

APPLICANT: Ruben, Steven, M.

TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10

FILE REFERENCE: 1488.115000C

CURRENT APPLICATION NUMBER: US 60/187,999

FRIOR APPLICATION NUMBER: US 60/187,999

FRIOR PILING DATE: 2000-03-09

FRIOR FILING DATE: 2000-09-22

NUMBER OF SEQ ID NOS: 58

SOFTWARE: Patentin version 3.0

SEQ ID NO 9

LENGTH: 344
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Pred. No. 2e-150;
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100.0%; Pred. No. ...
0; Mismatches
             CURRENT APPLICATION NUMBER: US/09/179,879A
CURRENT FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: US 60/181,258
PRIOR FILING DATE: 2000-02-09
PRIOR FILING DATE: 2000-03-09
PRIOR FILING DATE: 2000-03-09
PRIOR FILING DATE: 2000-03-09
PRIOR FILING DATE: 2000-03-09
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 58
SOFTWARE: Patentin version 3.0
SEQ ID NO 9
REFERENCE: 1488.115000A
                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 344; Conservative
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US-09-779-879A-9
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APPLICANT: Li, Yi
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Human G-Protein Chemokine Receptor (CCR5) HDGNR10
FILE REFERENCE: 1488.11500N
CURRENT APPLICATION NUMBER: US/10/232,686
CURRENT FILING DATE: 1999-06-23
FRIOR APPLICATION NUMBER: 09/339,912
FRIOR PILING DATE: 1999-06-25
FRIOR PILING DATE: 1999-06-25
FRIOR PILING DATE: 1999-06-26
FRIOR FILING DATE: 1999-06-06-29
FRIOR FILING DATE: 1999-06-06
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   92.5%; Score 1823; DB 9;
Query Match 92.5%; Score 1823; DB 9; Best Local Similarity 100.0%; Pred. No. 2e-150; Matches 344; Conservative 0; Mismatches 0
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SOFTWARE: Patentin version 3.0
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RESULT 15
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                                                         301 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 344
                                            318 IALGCRIAPLOKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 361
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RESULT 14 US-10-135-839-9

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sequence 9, Application US/09725285;
sequence 9, Application US/09725285;
patent No. US20010000241A1
sequence 1, Vi
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                                                                                                                                APPLICANT: Rosen, Craig A.
APPLICANT: Roschke, Viktor
APPLICANT: Roschke, Viktor
APPLICANT: Roschke, Viktor
APPLICANT: Ruben, Steven, M.
TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10
FILE REFERENCE: 1488.115000A
CURRENT FILING DATE: 2002-05-01
FRIOR APPLICATION NUMBER: US/09/779,839
FRIOR APPLICATION NUMBER: US 60/187,999
FRIOR APPLICATION NUMBER: US 60/187,999
FRIOR APPLICATION NUMBER: US 60/234,336
FRIOR APPLICATION NUMBER: US 60/234,336
FRIOR PILING DATE: 2000-03-09
FRIOR PILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 58
SOFTWARE: PatentIn version 3.0
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Sequence 9, Application US/10135839 Publication No. US20030166024A1 GENERAL INFORMATION:
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Best Local Similarity 100.0
Matches 344; Conservative
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-135-839-9
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    PatentIn version 3.0
; SOFTWARE: Patentin; SEQ ID NO 9; LENGTH: 329; TYPE: PRT; TYPE: PRT; ORGANISM: Protein US-09-725-285-9
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Search completed: June 9, 2005, 17:06:37 Job time: 106.455 secs

Murine CC
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Mouse GPC
Mouse GPC
Rat Prote
Rat Prote
Amino aci
Human CCR

Aaw27123 I Aaw27125 I Aaw23835 I Aaw88232 I

Aag80111 Aae04321

Aab83354 Aab82948 Aam52828 Abb08343

Adp74040
Aab46859
Adr16266
Adc29228
Adw54037
Adw44859
Add44859
Add44863
Adw27407
Aaw27407

Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

Database

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Monocyte chemoattractant protein-1 receptor; MCR-1R; chemokine
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/label= extracellular
49. .70
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(REGC ) UNIV CALIFORNIA.
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29-DEC-1995
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             GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                     2105692 segs, 386760381 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                - protein search, using sw model
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AAG80108
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                         degenerate oligo primers were designed corresp. to the conserved sequences R79167 in the second and R79168 in the third transmembrane domains of the MIP-lalpha/RANTES receptor, the IL-8 receptors and the HWGTRS corptor to the conserved sequences R79167 in the second and R79168 in the third transmembrane commands of the MIP-lalpha/RANTES receptor, the IL-8 receptors and the HWGTRS corptor are copied as the IL-8 receptors and the HWGTRS corporating EcoRI and XhoI sites at their 5' ends are 096299 and incorporating EcoRI and XhoI sites at their 5' ends are 096299 and incorporating EcoRI and XhoI sites at their 5' ends are 096299 and incorporating EcoRI and Adrived from MMG cells with the primers yieled a number of ECR products. One CDNA appeared to encode a novel protein. To obtain a full-length version of this clone, a MMG cDNA library was constructed in pERGG and probed with the PCR product. A 2.1 kb cDNA clone was obtd. Analysis of additional clones in the MMG cDNA library revealed a second sequence that was identical to the 2.1 kb cDNA sequence first obtd. From the 5' UTR through the putative seventh sequence from how contained a different cytoplasmic tail. The second sequence appears to represent alternative splicing of the carboxyl terminal tail of the MCP-IR protein. The two sequences are denoted MCP-terminal tail of the MCP-IR protein. The two sequences are denoted MCP-IR has a predicted mol. wt. of about 42,000 daltons. MCP-IRB has a mol. correct PN
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                                                                                                                             To identify and clone new members of the chemokine receptor gene family,
                             DNA encoding monocyte chemo-attractant protein-1 receptor - used parti
for identifying antagonists and for treating diseases characterised by
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iive 0; Mismatches 0;
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                                                                                               Claim 2; Fig 2; 84pp; English.
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DNA encoding human monocyte chemoattractant protein 1 receptor - used to treat tumours and inflammatory, viral, infectious, allergic, diabetic and central nervous system diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 1900; DB 2; Best Local Similarity 100.0%; Pred. No. 1.9e-206; Matches 360; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 12-14; 15pp; Japanese.
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                                                                                                                                                                                     96JP-00053574
                                                                                                                                                                                                                                                    96JP-00053574
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                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAT96976.
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Homo sapiens
                                                           JP09238688-A
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                                                                                                                                                                                                                                                11-MAR-1996;
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AAU07614 standard; protein; 360 AA
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                                                                                                                                                                                                                                                                                                      This invention describes a novel diagnostic agent (A) comprising at least two different ligands (I) for receptors (II) that are implicated in disease. (A) are used for the diagnosis of tumors (especially colorectal or prostatic), organ rejection, inflammation and autoimmune diseases. Also inhibitors of (I) are used therapeutically against tumors (and their metastases), inflammation (particularly bronchial asthma or chronic bowel inflammation), or autoimmune diseases (rheumatoid arthritis or lupus), where the (cardio) vascular, lymphatic, respiratory, nervous, disestive, endocrine, motor or urogenital systems or skin are affected, and bone (marrow diseases. The products of the invention are chemokine derivatives which have cytostatic, antiinflammatory, antisathmatic, immunosuppressive, dermatological, antirheumatic, antiarthritic.

Chemokines act on specific tumor and inflammatory cells through a constellation of these cells. Ad880045-A4880128 represent human chemokine fragments used to illustrate the method of the invention
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                                                                                                                                                                                                                            Diagnostic agent containing two or more receptor-specific ligands, useful for detecting tumors, inflammation etc., also therapeutic use of ligand inhibitors.
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                                                                                                                                                                          Spodsberg N;
                                                                                                                                                                       Heitland A,
                                                                                                                                                                                                                                                                                 Disclosure; Page 9; 26pp; German.
                                                                               02-APR-2001; 2001WO-EP003708
                                                                                                        31-MAR-2000; 2000DE-01016013
                                                                                                                                                                         Forssmann W, Adermann K,
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                                                                                                                                 (IPFP-) IPF PHARM GMBH. (FORS/) FORSSMANN U.
                                                                                                                                                                                                WPI; 2001-626256/72.
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wes 360; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 360 AA;
                        40200172830-A2
 Homo sapiens
                                                    04-OCT-2001
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RESULT 4

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The invention relates to diagnosing atherosclerosis (or susceptibility to) in a subject by determining expression or activity of the human CCR2-61 polypeptide (a polymorphic variant form of the human CCR2-fet propertied (a polymorphic natiant form of the human CCR2-fet polymorphic mucleotide polymorphic min codon 64 of the polymorleotide encoding the CCR2-fet polymorphism in codon 64 of the polymorleotide encoding polymorphic variants are associated with a lower incidence of atherosclerosis. The presence or amount of CCR2-fet polymorphic variants are supences of the invention can be used for also be analysed. The sequences of the invention can be used for predicting the response of a patient to drug treatment, for predicting the disease outcome in a patient and also for the production of a treatment for hypercholesterolaemia. The sequence represents the wild-type receptor polypeptide CCR2-64V
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                                                                         Human, CCR2 receptor, CCR2-641, CCR2-64V, gene therapy, atherosclerosis,
single nucleotide polymorphism; hypercholesterolaemia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Diagnosing atherosclerosis or susceptibility to atherosclerosis in a subject, by determining a single nucleotide polymorphism in specific codon of a polynucleotide encoding human CCR2 receptor in genome of t
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Human wild-type CCR2-64V polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 21; 28pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                22-FEB-2001; 2001WO-GB000755.
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                                                                                                                                                                                            Homo sapiens
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241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents human chemokine receptor CCR2. The specification describes a method for modulating viral infection of a cell. the method comprises modulating a binding interaction between a cell chemokine-receptor and a surface protein of the virus. The proviso is that the cell chemokine-receptor is not CX3CR1 and that the virus is not HIV. The method is useful for treating or preventing respiratory virus infection in vertebrates, more particularly respiratory syncytial virus (RSV) infections, and related diseases, e.g. bronchiolitis, bronchitis, pneumonia or asthma
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                                                       301 NPIIYAFVGEKFRYLSVFFRKHITKRFCKOCPVFYRBTVDGVTSTNIPSTGEOEVSAGL
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                                                                                                                                                                                                                                                                                            Human, chemokine receptor, CCR2, viral infection, surface protein,
respiratory virus infection, respiratory syncytial virus infection,
RSV infection; bronchiolitis, bronchitis, pneumonia, asthma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modulating viral infection of a cell, for treating or preventing respiratory virus infections, bronchitis, pneumonia or asthma, by modulating a binding interaction between a cell chemokine-receptor
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                                                                                                                                                                                                                                                             Amino acid sequence of human chemokine receptor CCR2.
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                                                                                                                                                         ABP97725 standard; protein; 360 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                surface protein of the virus.
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                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TOPI-) TOPIGEN PHARM INC.
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Matches 360; Conservative
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N-PSDB; ABZ68878.
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                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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The present invention describes antigenic peptides (I) comprising: (a) any one of 1601 sequences (see ABPR2019 to ABPR3019) of 12-24 amino acids. Also described: (1) an assay for the detection of a particular G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample; and (2) an isolated antibody having high specificity and high affinity or avidity for a particular GPCR. (I) can be used as GPCR modulators and in gene therapy. The antigenic peptides for GPCRs are useful in detecting an antibody against a particular GPCR, and in the production of specific presence or absence of corresponding GPCRs. The antigenic peptides for GPCRs and antibodies are useful for diagnosing and designing drugs for treating immune-related diseases, growth-related ciseases, cell regeneration-related diseases, growth-related ciseases, cell regeneration-related diseases, e.g. AIDS, Alzheimer's disease,
240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     G protein-coupled receptor; GPCR; antigenic peptide; gene therapy; G protein-coupled receptor modulator; antibody; immune-related disease; growth-related disease; call regeneration-related disease; AIDS; cancer; immunological-related cell proliferative disease; autoimmune disease; Alzheimer's disease; atherosclerosis; infection; osteoarthritis, allergy; osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes; graft versus host disease; Parkinson's disease; multiple sclerosis; pain; psoriasis; anxiety; depression; schizophrenia; dementia; memory loss; mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea; hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated antigenic peptides e.g., for G protein-coupled receptors (GPCR), useful for diagnosing and designing drugs for treating conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
                                                                                                                                                                                                                                                                                                                                                                                                      301 NPIIYAFVGEKFRRYLSVFPRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL
                                                                                                                                                                         241 AVRVIFTIMIVYFLFWTPYNIVILLINTFQBFFGLSNCESTSQLDQATQVTFTLGMTHCCI
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                osteoarthilis, osteoporosis, cancer, cardiomyopathy, chronic and acute inflammation, allargies, Crohn's disease, diabetes, graft versus host disease, Parkinson's disease, multiple sclerosis, pain, psoriasis, anxiety, depression, schizophrenia, dementia, mental retardation, memory loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension, hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or any other disorder in which GPCRs are involved. The antibodies may be used in immunoassays and immunodiagnosis. ABZ41281 to ABZ42869 encode GPCR proteins given in ABP81675 to ABP82018, which are used in the exemplification of the present invention
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atherosclerosis, bacterial, fungal, protozoan or viral infections,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human; adipocyte specific; adipose tissue; anti-obesity; high mobility group I-C protein; HMGI-C; obesity; leptin; ob; adipogenesis; hypertension; cardiovascular disease; anorectic; antidiabetic; hypotensive; chemokine (C-C) receptor 2.
                                                                                                                                                                                                                                                                         Length 360;
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100.0%; Pred. No. 1.9e-206;
tive 0; Mismatches 0;
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12-JUN-2003; 2003US-0478206P.
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Matches 360, Conservative
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This invention relates to a novel method for identifying genes that are over-expressed in adipose tissue and as such it provides targets for anticobesity pharmaceutical compositions. Specifically, it refers to a high mobility group I-C protein (HWG1-C) that is associated with obesity and is epistatic to leptin, furthermore, it refers to the ob gene where an autosomal recessive trait is linked to obseity and diabetes. The present invention describes performing differential gene expression analysis between the white adipose tissue (WAT) or stromal vascular tissue (SVT) or invention describes performing differential gene expression analysis between the white adipose tissue (WAT) or stromal vascular tissue (SVT) or invention describes and the encoded proteins thereof were this method novel nucleotides and the encoded proteins thereof were denoted and adiposences specific, and as such can be used for preventing adipogenesis, diagnosing and treating diabetes, obesity, these compositions exhibit anorectic, antidiabetic and cobesity. These compositions exhibit anorectic, antidiabetic and obesity. These compositions exhibit anorectic, antidiabetic and chapter of a murine adipocyte specific protein sequence of the invention.
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                                                                   Identifying adipocyte specific genes, useful for treating obesity or diabetes, and for identifying drug targets, by differential gene expression analysis between adipose tissue or stromal vascular tissue of mice of different genotypes.
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                                                                                                                                                                                       Disclosure; SEQ ID NO 579; 91pp; English
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Matches 360; Conservative
WPI; 2004-143846/14.
N-PSDB; ADM66946.
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AAU07613 standard; protein; 360 AA.
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                                                                       AAU07613;
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                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to PRO proteins and their coding sequences.

The PRO proteins are useful for diagnosing and treating a B cell related disorder, e.g. X-linked infantile hypogammaglobulinemia, polywaccharide antigen unresponsiveness, selective IgA deficiency, selective IgA deficiency with hypersensitivity, rheumatoid arthritis, autoimmune mediated haemolytic anaping, expondylitis. The PRO proteins are also useful separes The PRO coding sequences are useful as hybridization probes in chromosome and gene mapping, in preparing PRO proteins, or in generating transgenic animals or knockout animals, which in turn are useful in the development and screening of therapeutically useful reagents.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                New PRO polypeptide, useful for diagnosing and treating a B cell related disorder, e.g. Burkitt's lymphoma, rheumatoid arthritis, autoimmune mediated hemolytic anemia, myasthenia gravis or ankylosing spondylitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 CQXEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKRRHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGWTHCCI
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                                                                                                                                                                                                          Fong S, Schoenfeld JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 1900; DB 8;
100.0%; Pred. No. 1.9e-206;
ive 0; Mismatches 0;
immune-mediated inflammatory disease; human.
                                                                                                                                                                                                                                                                                                                                                             Claim 10; Fig 33; 695pp; English
                                                                                                                   15-SEP-2003; 2003WO-US029097
                                                                                                                                                 16-SEP-2002; 2002US-0411392P
                                                                                                                                                                                                          Clark H, Dennis K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.
Matches 360; Conservative
                                                                                                                                                                             (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                      WPI; 2004-329389/30.
N-PSDB; ADL82830.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 360 AA;
                                                         WO2004024097-A2
                             Homo sapiens
                                                                                       25-MAR-2004
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In some production of CCR2-form of the production of the producting form of the sequences of the invention can be used for predicting the response of a patient to drug treatment, for predicting the disease outcome in a patient and also for the production of a patient and also for the production of a treatment for hypercholesterolaemia. The sequence represents the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120
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                                                                                                                                   Human, CCR2 receptor, CCR2-641, CCR2-64V, gene therapy, atherosclerosis,
single nucleotide polymorphism, hypercholesterolaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Diagnosing atherosclerosis or susceptibility to atherosclerosis in a subject, by determining a single nucleotide polymorphism in specific codon of a polynucleotide encoding human CCR2 receptor in genome of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN
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Pred. No. 2.4e-206;
1; Mismatches 0;
                                                                     Human CCR2-64I polymorphic variant polypeptide.
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                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 20; 28pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-FEB-2000; 2000GB-00004183.
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al Similarity 99.7%;
359; Conservative
(first entry)
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N-PSDB; AAS12139.
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Matches 359; Conserv
                                                                                                                                                                                                                                                                                                                                                  Misc-difference 64
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180

300 300 360

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The invention describes an isolated polynucleotide comprising a sequence encoding the polypeptide comprising a 355 residue amino acid sequence, given in the specification, a sequence encoding the polypeptide expressed by the DNA contained in ATCC Deposit No. 97187, a sequence that hybridises with, or that is at least 70 % identical to them, or a sequence fragment of them. The polynucleotide is useful for preparing a composition for diagnosing or treating asthma, acute heart failure, hypertension, osteoporosis, allergies, dementia or ulcers. This is the amino acid sequence of human monocyte chemoattractant protein 1 receptor starting at residue 40 and used in a comparison with human G protein
                                                                                                                                                                                                                       301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polynucleotide, useful for preparing a composition for diagnosing or treating e.g. asthma, acute heart failure, hypertension, osteoporosis,
                 121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK
                                                                                  181 CQKEDSVYVCGPYFPRGMNNFHTIMRNIIGLVLPLLIMVICYSGIIKTLLRCRNEKKRHR
HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK
                                                                 COKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR
                                                                                                                                  AVRVIPTIMIVY PLEWTPYNIVILLINTPQEFFGLSNCBSTSQLDQATQVTBTLGMTHCCI
                                                                                                                                                                  241 AKRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI
                                                                                                                                                                                                     NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                          antiasthmatic; cardiant; hypotensive; antiallergic; neuroprotective; osteopathic; vulnerary; gene therapy; asthma; acute heart failure; hypertension; osteoporosis; allergy; dementia; ulcer; human; grotein coupled receptor; HGBRR32; monocyte chemoattractant protein 1 receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 347;
                                                                                                                                                                                                                                                                                                                                                                                                                           Partial human monocyte chemoattractant protein 1 receptor.
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100.0%; Pred. No. 1.9e-199;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                        ADF56627 standard; protein; 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            allergies, dementia or ulcers.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JUN-2002; 2002US-00176078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95US-00461244
98US-00104792
                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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Best Local Similarity 100.
Matches 347; Conservative
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25-JUN-1998;
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121
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                               CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240
                                                                               300
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                                                                                                               241 AVRVIPTIMIVYFLFWIPYNIVILLNTPQEFFGLSNCESTSQLDQATQVTETLGWTHCCI 300
                                                                                                                                              301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL 360
                                                                                                                                                                    Identifying agonists of G protein-coupled receptors (GPCRs) for use in disease treatment, comprises contacting candidate compounds with versions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to G protein-coupled receptors (GPCRs) for which the endogenous ligand has been identified. Non-endogenous constitutively activated versions of known GPCRs are used in the invention for the direct identification of candidate compounds as receptor agonists, inverse agonists or partial agonists. Such agonists are useful as therapeutic agents for diseases or disorders associated with GPCRs. The present sequence is a non-endogenous version of a known human GPCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
            COKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR
                                                                             241 AVRVIFTIMIVYFLFWTPYNIVILLMTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI
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                                                                                                                                                                                                                                                                                                                                                                                                           receptor; GPCR; non-endogenous; mutant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1894; DB 4; Length 360;
Pred. No. 8.9e-206;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO: 473.
                                                                                                                                                                                                                                                                                                                                                                                                         Human; G protein-coupled receptor; GPCR; non-end constitutively activated GPCR; agonist; disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 274-275; 394pp; English.
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                                                                                                                                                                                                                                                                                                                                                                       Non-endogenous human GPCR protein,
                                                                                                                                                                                                                                                                   ABB56340 standard; protein; 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-APR-2001; 2001WO-US011098
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Best Local Similarity 99.7%;
Matches 359; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lehmann-Bruinsma K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-648759/74.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                            181
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            181
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                                      74 KCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIIL 133
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                1 NESGEEVITFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVPIFGFVGNMLVVLILINCKKG
                                                                              LTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVDGIIFTKCOKEDSVYVCGPY
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                                                                                                             181 FPRGWNNFHTIMRNILGEVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYF
                                                                                                                                   LFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFR
        NESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVF1FGFVGNMLVVL1L1NCKKL
                                                                                                                                                                                                                                                                                              Monocyte chemoattractant protein-1 receptor; MCR-1R; chemokine.
                                                                                                                                                                 314 RYLSVFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL 360
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To identify and clone new members of the chemokine receptor gene family, degenerate oligo primers were designed corresp. to the conserved sequences R79167 in the second and R79168 in the third transmembrane domains of the MIP-lalpha/RANTES receptor, the IL-8 receptors and the HUMSTRS orphan receptor (GenBank Accession #M99293. The degenerate oligo incorporating ECORI and XhoI sites at their 5' ends are (96299 and conspired) any mapper of CDNA derived from MM6 cells with the primers yieled a number of FCR products. One CDNA appeared to encode a novel protein. To obtain a full-length version of this clone, a MM6 CDNA library was constructed in pFROG and probed with the PCR product. A 2.1 kb cDNA clone was obtd. Analysis of additional clones in the MM6 CDNA library revealed a second sequence that was identical to the 2.1 kb cDNA clone was obtd. Analysis of additional the puterive seventh transmembrane domain but contained a different cytoplasmic tail. The second sequence appears to represent alternative splicing of the carboxyl terminal tail of the MCP-IR protein. The two sequences are denoted MCP-IR has a predicted mol. Wt. of about 42,000 daltons. MCP-IRB has a mol. Wt. of about 42,000 daltons. Correct PN engles and predicted mol. Wt. of about 42,000 daltons. Correct PN
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DNA encoding monocyte chemo-attractant protein-1 receptor - used partic. for identifying antagonists and for treating diseases characterised by monocytic infiltrates.
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Matches 319; Conservative
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This invention describes a novel diagnostic agent (A) comprising at least two different ligands (I) for receptors (II) that are implicated in disease. (A) are used for the diagnosis of tumors (especially colorectal or prostatic), organ rejection, inflammation and autoimmune diseases.

Also inhibitors of (I) are used therapeutically against tumors (and their metastases), inflammation (particularly bronchial asthma or chronic bowel inflammation), or autoimmune diseases (rheumation, respiratory, nervous, diseases), and or inflammation, worth or urogenital systems or skin are affected, and bone marrow diseases. The products of the invention are chemokine derivatives, which have cytostatic, antiinflammatory, antiathmatic, which have cytostatic, antiinflammatory, antiathmatic, antiarthritic.

Chemokines act on specific tumor and inflammatory cells through a constellation of chemokine receptors (CR), which control migration and proliferation of these cells. Adg80045-AA0680128 represent human chemokine fragments used to illustrate the method of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                       Diagnostic agent containing two or more receptor-specific ligands, useful for detecting tumors, inflammation etc., also therapeutic use of ligand
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chronic bowel inflammation; rheumatoid arthritis; cytostatic; antiinflammatory; antiasthmatic; immunosuppressive; dermatological; antirheumatic; antiarthritic.
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3; Mismatches 5;
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Matches 319; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to nucleic acids encoding the chemokines TECK, MIP-3alpha, MIP-3beta, DC CR and M/DC CR. The polypeptide sequences are useful in isolating DNA clones encoding the chemokines, for generating antibodies, and for predicting oligonucleotides for screening a library to isolate species variants. A nucleic acid encoding a chemokine polypeptide can be used to identify genes, mRNA and cDNA species which encode related or homologous ligands, as well as DNA encoding homologous proteins from different species. The chemokines and antibodies which bind to the polypeptides are useful in the treatment of conditions associated with abnormal physiology or development, including inflammatory conditions such as asthma, abnormal proliferation, regeneration, degeneration and atrophy. This sequence represents the human chemokine receptor-2 (CKR-2) polypeptide, used in the scope of the invention
                                                                                                                                                                 Human, thymus expressed chemokine; TECK; chemokine; MIP-3alpha; receptor; MIP-3beta; dendritic cell receptor for chemokine; DC CR; M/DC CR; asthma; moncyte/dendritic cell receptor for chemokine; inflammatory condition; abnormal proliferation; degeneration; atrophy; antinflammatory; antiasthmatic; cytostatic; chemokine receptor-2; CKR-2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 MLVVLILINCKKLKCITDIYLLNIAISDLLFLITLPLWAHSAANBWVFGNAMCKLFTGLY 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New chemokines, TECK, MIP-3 alpha, MIP-3 beta, DC CR and M/DCCR, useful for treating conditions associated with abnormal physiology or development, including inflammatory conditions (e.g. asthma), and abnormal proliferation.
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95.5%; Pred. No. 3.1e-178;
iive 3; Mismatches 5;
                                                                                                                               Human chemokine receptor-2 (CKR-2) polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vicari A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 9-10; 54pp; English.
                 ABU09083 standard; protein; 374 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                       96US-0021664P.
96US-0028329P.
97US-0048593P.
97US-00887977.
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                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SCHE ) SCHERING CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-416900/39.
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                                                                                                                                                                                                                                                                                                                          JS2003018167-A1.
                                                                                                                                                                                                                                                                                      Homo sapiens
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04-JUN-1997;
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ABU09083
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The invention discloses a composition comprising two or more isolated rate or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the nucleic acid sequence. Also claimed are a vector, a method for identifying a nucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially respressed in an animal subjected to pain and a first that increases or decreases the expression of the polynucleotide sequence that increases or decreases the expression of the polynucleotide sequence that increases or decreases the expression of a polynucleotide sequence which is differentially expressed in neuronal tissue of a first animal compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the cutvity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more
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240
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                                                                                                                                                  241 AVRVIFTIMIVYFLFWTPYNIVILLANTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
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                                                                              181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR
                                                                                                                                 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; pain; neuronal tissue; gene therapy;
spinal segmental nerve injury; chronic constriction injury; CCI;
spared nerve injury; SNI; Chung.
                                                                                                                                                                                                      301 NPIIYAFVGEKFRYLSVFFRKHITKRFCKQCPV 334
                                                                                                                                                                                                                             301 NPIIYAFVGEKFR---SLF---HIALG-CRIAPL 327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human Protein P41597, SEQ ID NO 10292.
                                                                                                                                                                                                                                                                                                                                      ADD44861 standard; protein; 374 AA
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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(FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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95.5%; Pred. No. 3.1e-178;
ive 3; Mismatches 5; Indels
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Matches 319; Conservative
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Job time: 112.826 secs
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GenCore version 5.1.6
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- protein search, using sw model OM protein

June Run on:

9, 2005, 16:29:43 ; Search time 25.0136 Seconds (without alignments) 1384.767 Million cell updates/sec

US-10-791-166-4 Perfect score:

1900 1 MLSTSRSRRPIRNTNESGEEV......DGVTSTNTPSTGEQEVSAGL 360 Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB E Maximum DB E

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	chemokine (C-C) re	chemokine (C-C) re	chemokine (C-C) re	chemokine (C-C) re	MIP-1 alpha recept	•—	chemokine (C-C) re	chemokine (C-C) re	chemokine (C-C) re	G protein-coupled	MIP-1 alpha recept	G protein-coupled	probable G protein	orphan G protein-c	chemokine receptor	lymphocyte-specifi	G protein-coupled	G protein-coupled	G protein-coupled	interleukin-8 rece	interferon-inducib	G protein-coupled	interleukin-8 rece	fusin (LESTRA) - c	neuropeptide Y/pep				
SUMMARIES		443	450	113	177	341	339	436	587	160	594	340	190	186	304	942	735	735	680	890	611	231	921	752	960	349	989	445	048	787
	GI	JC2443	I38450	A43113	A45177	149341	I49339	G02436	JC4587	A57160	855594	I49340	JC5067	158186	JC4304	JC5942	B55735	A55735	A45680	JC5068	A53611	301231	A48921	A53752	842096	JE0349	I65989	A39445	G0004	828
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	Length	360	374	352	355	359	355	355	360	360	383	356	355	354	355	344	378	378	378	369	360	355	359	358	356	367	333	350	352	353
de	Query	100.0	86.9	71.8	54.5	53.2	50.7	50.1	45.8	45.4	4	41.0	39.5	ë		34.2	30.6	29.9	29.9	29.6	28.8	28.4	28.4	28.2	28.0	œ	27.8	~	27.1	27.1
	Score	1900	1651.5	1364	1036	1010.5	963.5	951	871	862.5	822.5	778.5	751	722.5	708	649.5	581.5	569	. 567.5	563	547	540.5	540.5	536.5	532.5	532	2	æ	15.	515
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neuropeptide Y/pep	G protein-coupled	angiotensin II rec	angiotensin II rec	G protein-coupled	H	II	andiotensin II rec	H	angiotensin II rec	angiotensin II rec	II	angiotensin II rec	G protein-coupled	MDCR15 protein - h	G protein-coupled
A45747	JN0621	S15403	A42656	S42628	JC2134	JC1104	S44425	JH0621	JQ1516	JC1194	151372	A48857	S32785	856162	S26667
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352	350	359	359	374	359	359	359	359	359	359	359	359	374	327	372
27.0	26.1	25.6	25.3	25.3	25.0	25.0	25.0	24.9	24.8	24.7	24.7	24.5	24.5	24.5	24.5
512.5	495.5	486.5	480.5	480	475.5	474.5	474.5	472.5	471.5	469.5	468.5	466	465.5	465	465
30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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C;Species: Homo sapiens (man)
C;Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 09-Jul-2004
C;Accession: JC2443; I38463
R;Yamagami, S.; Tokuda, Y.; Ishii, K.; Tanaka, H.; Endo, N.
Biochem. Biophys. Res. Commun. 202, 1156-1162, 1994
A;Title: cDNA cloning and functional expression of a human monocyte chemoattractant prote
A;Reference number: JC2443; MUID:94324942; PMID:8048929
                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-360 <YAM>
A; Cross-references: UNIPROT: P41597; DDBJ: D29984; NID: g531246; PIDN: BAA06253.1; PID: g53124
A; Cross-references: UNIPROT: P41597; DDBJ: D29984; NID: g531246; PIDN: BAA06253.1; PID: g53124
A; Cross-references: UNIPROT: P41597; DDBJ: D29984; NID: g531246; PIDN: BAA06253.1; PID: g53124
B; Coconstance and Sci. U.S. A. 91, 2752-2756, 1994
A; Reference number: A53477; MUID: 94195821; PMID: 8146186
A; Reference number: A53477; MUID: 94195821; PMID: 8146186
A; Restautes: preliminary
A; Rocious type: mRNA
A; Residues: 1-360 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GDB:337364; OMIM:601267
A;Map position: 3p21-3p21
C;Superfamily: vertebrate rhodopsin
C;Superfamily: vertebrate rhodopsin
C;Superfamily: vertebrate splicing; G protein-coupled receptor; glycoprotein; transmembrane
F;43-70/Domain: transmembrane #status predicted <TM1>
F;81-100/Domain: transmembrane #status predicted <TM2>
chemokine (C-C) receptor 2, splice form B - human N; Alternate names: C-C CRR-2; monocyte chemoattractant protein 1 receptor; monocyte chemo
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F;154-12W/Domain: transmembrane #status predicted <TM4>
F;207-226/Domain: transmembrane #status predicted <TM5>
F;244-268/Domain: transmembrane #status predicted <TM6>
F;287-309/Domain: transmembrane #status predicted <TM6>
F;1418.binding site: carbohydrate (Abn) (covalent) #status predicted 
F;113-190/Disulfide bonds: #status predicted
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100.0%; Pred. No. 1.6e-156;
ive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 360; Conservative
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Qy 301 NPIIYAFVGEKFRYLSVFFKHITKRFCKQCPV 3.	A; Accession: A43113 A; Molecule trype: mRNA A; Residues: 1-32 < < SAM1. A; Cross-references: GB: X91492; NID: G1262810; PIDN: R; Samson, M.; Libert, F.; Doranz, B.J.; Rucker, J. R; Samson, M.; Libert, F.; Doranz, B.J.; Rucker, J. M.; Imai, T.; Rana, S.; Yi, Y.; Smyth, R.J.; Colling at 172-725, 1996 A; Title: Resistance to HIV-1 infection in caucasia A; Reference number: S71808 A; Status: nucleic acid sequence not shown; not com A; Molecule trype: DNA A; Residues: 182-206;207-230 < SAM2> A; Accession: A58314 A; Residues: 182-206;207-230 < SAM2> A; Residues: 182-206;207-230 < SAM2> A; Residues: 1982-206;207-230 < SAM2> A; Residues: 1982-206;207-230 < SAM2> A; Residues: GB: X99393; NID: G1524062; PIDN: A; Note: this frameshift mutation results in a non-nd may have had a selective advantage by conferring any have had a selective advantage by conferring A; Itle: Cloning and functional expression of CC A; Reference number: A58832; MUID: 96295970; PMID: 8; Accession: A58832 A; Molecule trype: mRNA A; Residues: 1-32 < COM1> A; Cross-references: GB: U57840; NID: G1502408; PIDN: A; Reperimental source: clone 8, endotoxin-stimulate A; Accession: GD: G3 A; Accession: GB: Data Library, May 1996 A; Accession: GD: G3 A; Accession: GD: G3 A; Accession: GD: G3 A; Accession: GD: G3 A; Reference number: H01541 A; Accession: GD: G3 A; Accession: GD: GD: GD: GD: GD: GD: GD: GD: GD: GD	A; Status 1 1892. A; Status 1 1894. A; Status 1 1894. A; Status 1 1894. L; 31-352 < CCM2> A; Residues: 1 1894. L; 31-352 < CCM2> A; Crosa-references: EMBL: U57840 B; Raport, C. U.; Gosling, U.; Schweickart, V.L.; Gr J; Biol. Chem. 271, 17161-17166, 1996 A; Title Molecular cloning and functional characte A; Reference number: A58833; MUID:96291862; PMID:86 A; Residues: 1-352 < RAP> A; Residues: 1-352 < RAP> A; Cross-references: GB:U54994; NID:g1457945; PIDN: A; Residues: U. Status 1 1805. CKR-5; CKR-5; CCMM-1 1805. CKR-5;
Qy 121 HIGYFGGIFFILLTIDRYLAIVHAVFALKARTVTFGVVTSVITMLVAVFASVFGIIFTK 180 Db 121 HIGYFGGIFFILLTIDRYLAIVHAVFALKARTVTFGVVTSVITMLVAVFASVFGIIFTK 180 Qy 181 CQKEDSVYVCGFYFFGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLARCKNEKKRHR 240 Db 181 CQKEDSVYVCGFYFFGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLARCKNEKKRHR 240 QY 241 AVRVIFTIMIVYFLFWTPYNIVILLMTFQBFFGLSNCSTSQLDQATQVTFTLGMTHCCI 300 Db 241 AVRVIFTIMIVYFLFWTPYNIVILLMTFQBFFGLSNCSTSQLDQATQVTFTLGMTHCCI 300 QY 301 NPIIYAFVGEKFRRYLSVFFKHITKRFCKQCPVFYRETVDGVTSTNTFSTGEQEVSAGL 360 Db 301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPVFYRETVDGVTSTNTFSTGEQEVSAGL 360 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	RESULT 2 IS8450 Chemokine (C-C) receptor 2, splice form A - human N;Alternate names: C-C CKR-2; monocyte chemoattractant protein 1 receptor; monocyte chemosite names: C-C CKR-2; monocyte chemoattractant protein 1 receptor; monocyte chemosite names: C-C CKR-2; monocyte chemoattractant proteins in 18450 C;Accession: I38450 R;Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R. A;Title: Molecular cloning and functional expression of two monocyte chemoattractant proteins: Nolecular cloning and functional expression of two monocyte chemoattractant proteins: Dreliminary A;Reference number: A53477; MUID:94195821; PMID:8146186 A;Status: preliminary A;Reference number: A53477; MUID:94195821; PMID:8146186 A;Status: preliminary A;Residues: 1-374 cKBS. A;Cross-references: UNIPROT:P41597; EMBL:U03882; NID:947255; PIDN:AAA19119.1; PID:94725 C;Genetics: answerbarate thodopsis: protein-coupled receptor; glycoprotein; transmembrane #status predicted <tm1. #status="" <tm3.="" <tm5.="" domain:="" f;115-1136="" f;124-1265="" f;292-309="" f;44-68="" f;59-99="" predic<="" predicted="" td="" transmembrane=""><td>Query Match 86.9%; Score 1651.5; DB 2; Length 374; Best Local Similarity 95.5%; Pred. No. 4.8e-135; Andels 7; Gaps 3; Matches 319; Conservative 3; Mismatches 5; Indels 7; Gaps 3; Qy IMLSTSRSRFIRNTNESGEEVTTFPDYDYGAPCHKFDVKQIGAQLLPPLYSLVPIFGFVGN 60 Db 1 MLSTSRSRFIRNTNESGEEVTTFPDYDYGAPCHKFDVKQIGAQLLPPLYSLVPIFGFVGN 60 Qy 61 MLVVLILINCKKLKCLTDIYLLNLAISDLFLITLPLWAHSAANEWVEGNAMCKLFTGLY 120 Db 61 MLVVLLILINCKKLKCLTDIYLLNLAISDLFLITLPLWAHSAANEWVEGNAMCKLFTGLY 120 Qy 121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVFGVVTSVITWLVAVFASVPGIIFTK 180 Qy 181 COKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240 Qy 241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQYTETLGMTHCCI 300 Db 241 AVRVIFTIMIVYFLFWTPYNIVILLANTFQEFFGLSNCESTSQLDQATQYTETLGMTHCCI 300</td></tm1.>	Query Match 86.9%; Score 1651.5; DB 2; Length 374; Best Local Similarity 95.5%; Pred. No. 4.8e-135; Andels 7; Gaps 3; Matches 319; Conservative 3; Mismatches 5; Indels 7; Gaps 3; Qy IMLSTSRSRFIRNTNESGEEVTTFPDYDYGAPCHKFDVKQIGAQLLPPLYSLVPIFGFVGN 60 Db 1 MLSTSRSRFIRNTNESGEEVTTFPDYDYGAPCHKFDVKQIGAQLLPPLYSLVPIFGFVGN 60 Qy 61 MLVVLILINCKKLKCLTDIYLLNLAISDLFLITLPLWAHSAANEWVEGNAMCKLFTGLY 120 Db 61 MLVVLLILINCKKLKCLTDIYLLNLAISDLFLITLPLWAHSAANEWVEGNAMCKLFTGLY 120 Qy 121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVFGVVTSVITWLVAVFASVPGIIFTK 180 Qy 181 COKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240 Qy 241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQYTETLGMTHCCI 300 Db 241 AVRVIFTIMIVYFLFWTPYNIVILLANTFQEFFGLSNCESTSQLDQATQYTETLGMTHCCI 300

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.ycoprotein; phosphoprotein; transmembrane<TM1>
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N:CAM67767.1; PID:91524063
m-functional receptor but confers a degre
ing resistance to Yersinia plague infecti
rphy, P.M.
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of HIV-1 bind to a complex of chemokine ((
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liferation and differentiation
                                                                                                                                                                                                                                                                                         sion of a new human CC-chemokine receptor
8639485
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J.; Liesnard, C.; Farber, C.M.; Saragostj
llman, R.G.; Doms, R.W.; Vassart, G.; Paı
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ian individuals bearing mutant alleles of 8751444
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8699119
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ated peripheral blood monocytes
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653; A58833
G.; Parmentier, M.
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Best Local Similarity 50.4 Matches 199; Conservative
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Best Local Similarity 53.5
Matches 193; Conservative
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A;Title: Structure and functional expression of the human macrophage inflammatory 1 alph
A;Reference number: 155671; MUID:93240122; PMID:7683036
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C;Keywords: disulfide bond; G protein-coupled receptor; glycoprotein; phosphoprotein;
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R;Neote, K.; DiGregorio, D.; Mak, J.Y.; Horuk, R.; Schall, T.J.
Cell 72, 415-425, 1993
A;Title: Molecular cloning, functional expression, and signaling characteristics of A;Reference number: A45177; MUID:93161416; PMID:7679328
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A;Experimental source: HL60 cells
A;Note: sequence extracted from NCBI backbone (NCBIP:124876)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
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F;67-87/Domain: transmembrane #status predicted <TM2>
F;103-124/Domain: transmembrane #status predicted <TM3>
F;142-166/Domain: transmembrane #status predicted <TM5>
F;142-166/Domain: transmembrane #status predicted <TM5>
F;236-257/Domain: transmembrane #status predicted <TM5>
F;285-300/Domain: transmembrane #status predicted <TM7>
F;285-300/Domain: transmembrane #status predicted <TM7>
F;20-269,101-178/Disulfide bonds: #status predicted <TM7>
F;20-269,103-178/Disulfide bonds: #status predicted <TM7>
F;20-269,101-178/Disulfide bonds: #status predicted <TM7-178/Disulfide Site: phosphate (Ser) (covalent) #status predicted <TM7-178/Disulfide Site: phosphate (Thr) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                Length 352;
                                                                                                                                                                                                                                                                              71.8%; Score 1364; DB 2; Length 3
75.5%; Pred. No. 3e-110;
ive 32; Mismatches 46; Indels
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A;Cross-references: GDB:138446; OMIM:601159
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A;Map position: 3p21-3p21
C;Superfamily: vertebrate rhodopsin
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Best Local Similarity 75.5%
Matches 259; Conservative
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mouse beta chemokir
F;36-60/Domain: transmembrane #status predicted <TM1>
F;71-91/Domain: transmembrane #status predicted <TM2>
F;71-91/Domain: transmembrane #status predicted <TM3>
F;108-129/Domain: transmembrane #status predicted <TM4>
F;147-171/Domain: transmembrane #status predicted <TM6>
F;240-264/Domain: transmembrane #status predicted <TM6>
F;240-264/Domain: transmembrane #status predicted <TM6>
F;280-305/Domain: transmembrane #status predicted <TM7>
F;581nding site: carbohydate (Asn) (Covalent) #status predicted
F;5410-131/Disulfide bonds: #status predicted
F;345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MIP-1 alpha receptor like-2 - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: 149341
R;Gao, J.L.; Murphy, P.M.
J;Biol. Chem. 270, 17494-17501, 1995
A;Fitle: Cloning and differential tissue-specific expression of three mouse
A;Reference number: 149339; MUID:95340546; PMID:7542241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KLKCLTDIYLLNLAISDLLFLITLPLWA-HSAANEWVFGNAMCKLFTGLYHIGYFGGIFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           191 GPYFP----RGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             12 NTNESGBEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 IRNTNESGEEVTTPPDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILIN
                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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A;Rosidues: 1.359 KRS>
A;Cross-references: UNIPROT:QBK3M7; EMBL:U28406; NID:g881551; PID:g881552
C;Superfamily: vertebrate rhodopsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     303 FVGERFRKYLRQLFHRRVAVHLVKWLPFLSVDRLERVSST-SPSTGEHELSAG 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FVGEKFRRYLSVFFRKHITKRFCKOCPVFYRETVDGVTSTNTPSTGEOEVSAG 359
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                                                                                                                                                                                                                                                                                                                                         Length 355;
                                                                                                                                                                                                                                                                                                                                   54.5%; Score 1036; DB 2; Length 3 56.4%; Pred. No. 6.4e-82; ive 56; Mismatches 90; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Accession: 149341
A,Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53.2%; Score 1010.5; DE 53.5%; Pred. No. 1e-79; ive 62; Mismatches 8
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A;Residues: 1-355 c-PON>
A;Cross-references: UNIPROT:P51677; EMBL:U49727; NID:g1477560; PIDN:AAB09726.1; PID:g1477; R;Combadiere, C.; Ahuja, S.K.; Murphy, P.M.
J. Biol. Chem. 270, 16491-16494, 1995
A;Title: Cloning and functional expression of a human eosinophil CC chemokine receptor.
A;Reference number: A57237; MUID:95348056; PMID:7622448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GDB:579624; OMIM:601268
A;Apap position: 3p21-3p21
C;Superfauily: vertebrate rhodopsin
C;Superfauily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane #status predicted <TM1>
F;36-60/Domain: transmembrane #status predicted <TM2>
F;10-91/Domain: transmembrane #status predicted <TM3>
F;108-129/Domain: transmembrane #status predicted <TM4>
F;40-521/Domain: transmembrane #status predicted <TM6>
F;40-521/Domain: transmembrane #status predicted <TM6>
F;28-305/Domain: transmembrane #status predicted <TM6>
F;28-305/Domain: transmembrane #status predicted <TM6>
F;28-31/Domain: transmembrane #status predicted <TM6>
F;28-31/Domain: transmembrane #status predicted <TM7>
F;38-31/Domain: transmembrane #status predicted <TM7>
F;38-31
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CiSpecies: Mus musculus (house mouse)
CiSpecies: Mus musculus (house mouse)
CiSpecies: Mus musculus (house mouse)
CiAccession: JG4887
R;Hoogewerf, A.J.; Black, D.; Proudfoot, A.B.I.; Wells, T.N.C.; Power, C.A.
Biochem: Biophys. Res. Commun. 218, 337-343, 1996
A;Title: Molecular cloning of murine CC CKR-4 and high affinity binding of chemokines to A;Reference number: JG4587; MUD:96136324; PMID:8573157
A;Molecule type: mRNA
A;Residues: 1-360 <HOO>
                                                                                                                                                                                                                                                                                                                                           A;Molecule type: mRNA
A;Residues: 1-106, N',108-275,'S',277-280,'R',282-355 <COM>
A;Residues: 1-106, N',108-64; NID:g1199579; PIDN:AACS0469.1; PID:g1199580
A;Note: the translated sequence in GenBank entry HSU28694, release 113.0, PIDN:AACS0469.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  256 WIPYNIVILLINTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRRY 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14 TSYYD-DVGELCEKADTRALMAQFVPPLYSEVFTVGELGRUVVVMILIKYRREKIMTNIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               197 -GWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLF
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50.1%; Score 951; DB 2;
Best Local Similarity 52.6%; Pred. No. 1.4e-74;
Matches 180; Conservative 65; Mismatches 89
                                                                                                                                                                                                                                                                                                              A;Status: nucleic acid sequence not shown
A;Accession: G02436
A;Status: translated from GB/EMBL/DDBJ
                                                                A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C,Genetics:
A,Gene: GDB:CMKBR3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  macrophage inflammatory protein-1 alpha receptor - mouse c;Species: Mus musculus (house mouse) C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004 C;Accession: 149339 P.M. Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004 C;Accession: Chem. 270, 17494-17501, 1995 A;Title: Chem. 270, 17494-17501, 1995 A;Title: Cloning and differential tissue-specific expression of three mouse beta chemoking A;Reference number: 149339; MUD:95340546; PMID:7542241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:P51675; EMBL:U28404; NID:g881547; PIDN:AAA89153.1; PID:g8815
C;Superfamily: vertebrate rhodopsin
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                                                                                                                                                                                                                                                                                          SCSPRYPEGEEDSWKRFHALRMNIPGLALPLLVMVICYSGIIKTLLRCPN-KKKHKAIRL 244
                                                                                                                             245 IFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCBSTSQLDQATQVTETLGMTHCCINPII 304
                                                                                                                                                          245 IFVVMIVFFIFWTPYNLVLLFSAFHSTFLETSCEQSKHLDLAMQVTEVIAYTHCCVNPVI 304
                                                                                                                                                                                                                                                    305 YAFVGEKFRRYLSVFFRKHITKRFCKQCPVFYRETV-----DGVTSTNTPSTGEQEV 356
      VCGPYFPRG----WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRV 244
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Chemokine (C-C) receptor 3 - human
NyAlternate names: C-C CRT-3
NyAlternate names: C-C CRT-3
C;Specides: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
C;Accession: G02436; A57237
R;Ponath, P.D.
R;Ponath, P.D.
R;Ponath, P.D.
A;Reference number: H01272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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F;183,194/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
                                                                  Query Match
Best Local Similarity 48.7%
Matches 164; Conservative
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Best Local Si
Matches 162
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A;Cross-references: UNIPROT:P51680; EMBL:X90862; N1D:gl10,021; F1DM:CLARGEST. A; Experimental source: thymus C;Genetics: C;Genetics: A;Gene: cc ckr-4
C;Superfamily: vertebrate rhodopsin C;Superfamily: vertebrate rhodopsin C;Keywords: glycoprotein; phosphoprotein; receptor; thymus C;Keywords: glycoprotein; phosphoprotein; receptor; thymus C;Keywords: glycoprotein; phosphoprotein; receptor; thymus F;2,183.194/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status pred F;18,2,202,350/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted F;321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;208-226/Domain: transmembrane #status predicted <TM5>
F;243-264/Domain: transmembrane #status predicted <TM6>
F;291-308/Domain: transmembrane #status predicted <TM7>
F;291-308/Domain: transmembrane #status predicted <TM7>
F;20-276.110-187/Disulfide bonds: #status predicted
F;72,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicte
F;145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
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A;Note: source clone K5-5
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A;Title: Molecular cloning and functional expression of a novel CC chemokine receptor o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane F;40-65/Domain: transmembrane #status predicted <TM1.>
F;76-97/Domain: transmembrane #status predicted <TM2.>
F;112-133/Domain: transmembrane #status predicted <TM3.>
F;112-133/Domain: transmembrane #status predicted <TM3.>
F;121-175/Domain: transmembrane #status predicted <TM4.>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    244
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                                                                                                                                                                                                                                                                                                                                                                                 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N;Alternate names: C-C CKR-4
C;Species: Homo sapiens (man)
C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: A57160
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VTDTTQDETVYNSYYFYESMPKPCTKBGIKAFGEVFLPPLYSLVFLLGLFGNSVVVLVLF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 IRNTNESGEEVITTFDYD-YGAPCHKFDVKOIGAQLLPPLYSLVFIFGFVGNMLVVLILI
                                                                                                                                                                                                                                                                                                                                                                                                                        NCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGI
                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  306 AFVGEKFRRYLSVFFRKHITKR----FCKQCPVFYRETVDGVTSTNTPSTGEQE 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12;
                                                                                                                                                                                                                                              Score 871; DB 2; Length 360;
Pred. No. 1.1e-67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                       71; Mismatches 103; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Reference number: A57160; MUID:95370289; PMID:7642634
A;Accession: A57160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (C-C) receptor 4 - human
                                                                                                                                                                                                                                              45.8%;
                                                                                                                                                                                                                                                                   Best Local Similarity 47.5%;
Matches 168; Conservative 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Map position: 3p21-3p21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-360 < POW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene: GDB: CMKBR4
                                                                                                                                                                                                                                                                                                                                                                                                                          69
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A;Cross-references: UNIPROT:Q89609; GB:U20824; NID:g695172; PIDN:AAC13788.1; PID:g695173
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    323
                                                                                                                                                                                            PLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLAIVHAVFALK 150
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S55594
S55594
Grotein-coupled receptor E1 - equine herpesvirus 2
C;Species: equine herpesvirus 2
C;Species: equine herpesvirus 2
C;Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
C;Accession. S55594
B;Telford, B.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.
J. Mol. Biol. 249, 520-528, 1995
A;Title: The DNA sequence of equine herpesvirus 2.
A;Reference number: S55594; MUID:95302501; PMID:7783207
                                                                                                PCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIYLLNLAISDLL
                                                                                                                                                                                                                                                                                                                                                                                                                208 ILGLVIPLGIMLFCXSMIRTLQHCKNEKK-NKAVKMIFAVVVLFLGFWTPYNIVLFLET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              267 LVELEVLQDCTFERYLDYALQATETLAFVHCCLNPIIYFFLGEKFRKYILQLFK---TCR
                                                                                                                         ARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG----WNNFHTIMRN
                                                                                                                                                                                                                                                                                                                                                                                       ILGLVLPLLIMVICYSGILKTLLRCRNEKRHRAVRVIFTIMIVYFLFWTPYNIVILLNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   268 POEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRRYLSVFFRKHITKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAH--SAANEWVFGNAMCKLFTGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 YHIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFT
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                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180 KCQKEDSVYVCGPYFP----RGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                 Indels
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                                                    95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; nucleic acid sequence not shown A;Molecule type: DNA
A;Residues: 1-383 <TEL>
    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43.3%; Score 822.5; DB 2;
llarity 47.9%; Pred. No. 1.9e-63;
Conservative 60; Mismatches 107;
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45.4%; Score 862.5; DB 2
48.7%; Pred. No. 6.1e-67;
iive 67; Mismatches 95
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probable g protein-coupled receptor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-011-1996 #sequence_revision 26-011-1996 #text_change 09-011-2004
C;Accession: ISB186
C;Accession: ISB186
A;Title: cDNA cloning of a G-protein-coupled receptor expressed in rat spinal cord and by A;Reference number: ISB186
A;Accession: ISB186
A;Accession: ISB186
A;Accession: ISB186
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;References unmber: ISB186
A;Coss-references: UNIPROT:P35411; EMBL:U04808; NID:g2558635; PIDN:AAB87093.1; PID:g4398
C;Superfamily: vertebrate rhodopsin
C;Keywords: G'protein-coupled receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             136 IDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFP 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 VTTFFDYDY ----GAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 VITVIDYXXPDIFSSPCDAELIQINGKLLLAVFYCLLFVFSLLGNSLVILVLVVCKKLRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                253 FLFWTPYNIVILLINTFOEFFGLSNCESTSQLDQATQVTETLGMTHCCINPILYAFVGEKF
                                                                                                                                                                                                                                                 A;Cross-references: EMBL:U45983; NID:g1245056; PID:g1245057
C;Comment: This protein belongs to the family of beta chemokine receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 313 RRYLSVFFRKHITKRF---CKQCPVFYRETVDGVTSTNTPSTGBQEV 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  308 KKHLSEIFQKSCSQIFNYLGRQMP---RESCEKSSSCQQHSSRSSSV 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tch 39.5%; Score 751; DB 2; Length 355; al Similarity 41.2%; Pred. No. 2.6e-57; 143; Conservative 69; Mismatches 121; Indels
                                                                                                                                                                                                                                                                                                                                                                                                 Gisuperfamily: vertebrate rhodopsin
Cisuperfamily: vertebrate rhodopsin
Cisuperfamily: vertebrate rhodopsin
Cistopanic Gistopanic recompled receptor; transmembrane protein
F;36-63/Domain: transmembrane #status predicted <TM1>
F;73-94/Domain: transmembrane #status predicted <TM2>
F;108-129/Domain: transmembrane #status predicted <TM3>
F;100-222/Domain: transmembrane #status predicted <TM5>
F;230-260/Domain: transmembrane #status predicted <TM5>
F;239-260/Domain: transmembrane #status predicted <TM5>
F;239-260/Domain: transmembrane #status predicted <TM5>
                       A, Cross-references: EMBL: U62556; NID: 91468978; PID: 91468979
                                                     RiBonner, T.I.
subnited to the EMBL Data Library, January 1996
A;Reference number: H01154
A;Accession: G02387
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Ablecule type: DNA
A;Residues: 1-355 <80N>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38.0%; Score 722.5;
                                                                                                                                                                                                                                                                                                                                              A;Gene: GDB:CMKBR8; CMKBRL2; TER1; CKR-L1
A;Cross-references: GDB:6053733; OMIM:601834
A;Residues: 1-355 <NAP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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Matches
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NyAlternate names: chemokine receptor-like protein TER1; GPR-CY6

C; Species: Home saptens (man)

C; Species: Home saptens (man)

C; Date: 31-Jan-1997 #sequence revision 31-Jan-1997 #text_change 09-Jul-2004

C; Date: 31-Jan-1997 #sequence revision 31-Jan-1997 #text_change 09-Jul-2004

C; Accession: UC5067; G02776; G02387

R; Raballos, A; Yarona, R.; Gutlerrez, J; Lind, P.; Marquez, G.

Bjochem. Bjophys: Res. Commun. 227, 846-883, 1996

A; Title: Molecular cloning and RNA expression of two new human chemokine receptor-like 9

A; Reference number: UC5067; MUID:97040707; PMID:8886020

A; Accession: UC5067

A; Accession: UC5067

A; Residues: 1-355 cAAB-

A; Residues: 1-355 cAAB-

A; Residues: L355 cAAB-

A; Cross-references: UNIPROT:P51685; EMBL:279782; NID:91668735; PIDN:CAB02142.1; PID:9166

R; Napolitano, M.; Zingoni, A.; Bernardini, G.; Spinetti, G.; Rocchi, M.; Santoni, A.

Bubbitted to the EMBL Data Library, June 1996
                                                                                                                                                                                                                                                                                                                         C;Accession: I49340
R;Gao, J.L.; Murphy, P.M.
Dislo. Chem. 270, 17494-17501, 1995
A;Title: Cloning and differential tissue-specific expression of three mouse beta chemoki
A;Title: Cloning and differential tissue-specific PMID:7542241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-356 <RES>
A;Cross-references: UNIPROT:P51676; EMBL:U28405; NID:g881549; PIDN:AAA89154.1; PID:g8815
C;Superfamily: vertebrate rhodopsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   144 HAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPR----GWN 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AISDLLFLITLPLWA-HSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLAIV 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18 DFWSGFLCFSINVRAFGITVPTPLYSLVFIIGVIGHVLVVLVLLQHKRLRNMTSIYLFNL 77
                                                                                                                                                                                                                                  MIP-1 alpha receptor like-1 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  200 NFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWTPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIYLLNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FRRHTAITLPOWLP-FLSEDRAGRASARLPSTVEIETSADL 356
                                                                 331 THCCINPVIYAFVGEKFRRHLYHFFHTYVAIYLCKYIP 368
                                THCCINPILYAFVGEKFRYLSVFFRKHITKRFCKQCP 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A, Accession: 149340
A, Status: preliminary; translated from GB/EMBL/DDBJ
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A;Accession: G02776
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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A;Cross-references: UNIPROT:000421; GB:U97123; NID:g2897070; PIDN:AAC39595.1; PID:g28970:
C;Superfamily: vertebrate rhodopsin
                                                                                                                     182 VLQEIWPVLRNVETNFLGFILPLLIMSYCYPRIIQTLFSCKNHKKA-KAIKLILLVVIVF 240
                                                                                                                                                                                                                                                                241 FLFWTPYNVMIFLETLKLYDFFPSCDMRKDLRLALSVTETVAFSHCCLNPLIYAFAGEKF 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLAIVH-A 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83 SNLCFLLTLPFWAHAG-----GDPMCKILIGLYFVGLYSETFFNCLLTVQRYLVFLHKG 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                146 VFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCOKEDSVYVCG----PYFPRG---W 198
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Cipate: 16-Jul-1999 #text_change 09-Jul-2004
Cipate: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
Cipatesion: JC5942
Righn, P.; Kyaw, H.; Su, K.; Zeng, Z.; Augustus, M.; Carter, K.C.; Li, Y.
Biochem. Biophys. Res. Commun. 243, 264-268, 1998
A; Title: Cloning and characterization of a novel human chemokine receptor.
A; Reference number: JC5942; MUID:98139902; PMID:9473515
A; Status: preliminary
A; Residues: 1-344 < FRAN;
A; Residues: 1-345 < FRAN;
A; 
                                                                            197 GWNNFHTIMRNI----LGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVY
                                                                                                                                                                                                                        FLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTFTLGMTHCCINPIIYAFVGEKF
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Job time: 27.0136 secs
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A;Experimental source: peripheral blood mononuclear cell
C;Comment: This protein is a cell-surface receptor which recognizes extracellular signal
C;Comment: This protein is a key regulator of many immune and homeostatic responses, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      t
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R;Raport, C.J.; Schweickart, V.L.; Eddy Jr., R.L.; Shows, T.B.; Gray, P.W.
Gene 163, 295-299, 1995
A;Title: The orphan G-protein-coupled receptor-encoding gene V28 is closely related
A;Reference number: JC4304; WUID:96011651; PMID:7590284
                                                                                                                                                                                                                                                     NLAISDLLFLITLPLWAHSAANBWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLAI 142
                                                                                                                                                                                                                                                                                          YNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRRYLSV 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 248 YNIVIFLETLKFYNFFPSCGMKRDLRWALSVTETVAFSHCCLNPFIYAFAGEKFRRYLRH 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TDIXLLNLALSDLLFVATLPFWTHYLINEKGLHNAMCKFTTAFFFIGFFGSIFFITVISI 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCOKEDSVYVCGPYFPR 196
                                                                                                             82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N;Âlternate names: V28 protein
C;Species: Homo sapiens (man)
C;Date: 16-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004
                                                                                                                                                      VHAVFALKARTVTFGVVTSVITWLVAVFASVPG11FTKCQKEDSVYVCGPYFPRGWNNFH
                                                                                                             FDYDYGA-PCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIYLL
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F; 66-88/Domain: transmembrane #status predicted <TM2>
F; 104-125/Domain: transmembrane #status predicted <TM3>
F; 146-165/Domain: transmembrane #status predicted <TM3>
F; 197-217/Domain: transmembrane #status predicted <TM5>
F; 197-217/Domain: transmembrane #status predicted <TM6>
F; 197-226/Domain: transmembrane #status predicted <TM6>
F; 230-254/Domain: transmembrane #status predicted <TM6>
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25-OCT-2004 (Rel. 45, Last annotation update)
2C chemokine receptor type 2 (C-C CKR-2) (CC-CKR-2) (CCR2)
(Monocyte chemoattractant protein 1 receptor) (MCP-1-R).
Name=CCR2; Synonyms=CMKBR2;
             2 (Potential).
Extracellular (Potential).
3 (Potential).
Cytoplasmic (Potential).
4 (Potential).
5 (Potential).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                    97.1%; Score 1845; DB 1; Length 360; 96.9%; Pred. No. 5.1e-106; ive 5; Mismatches 6; Indels
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Cytoplasmic (Potential)
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MEDLINE=94324942; PubMed=8048929;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SULPATION OF TYR-26, AND N-GLYCOSYLATION.
MEDLINE=20501139; PubMed=11046064;
Preobrazhensky A.A., Dragan S., Kawano T., Gavrilin M.A., Gulina I.V.,
Chakravarty L., Kolattukudy P., Ecceptor CR2B is a glycoprotein that
"Monocyte chemotactic protein-1 receptor CCR2B is a glycoprotein that
has tyrosine sulfation in a conserved extracellular N-terminal
                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDINES-9715084; PubMed=8995400; DOI=10.1074/jbc.272.2.1038;
MEDINES-97150864; PubMed=8995400; DOI=10.1074/jbc.272.2.1038;
MODINES-97150864; PubMed=8995400; Gosling J., Arai H., Charo I.F.;
"Organization and differential expression of the human monocyte chemoattractant protein I receptor gene. Evidence for the role of the carboxyl-terminal tail in receptor trafficking.";
J. Biol. Chem. 272:1038-1045(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D., Nhan M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K., Gnoj L., la Bastide M., Kaplan N., Greco T., Touchman J., Muzny D., Chen C.N., Bvans C., Fitzgerald M., See L.H., Tang M., Porcel B.M., Dragan Y., Giacalone J., Pae A., Powell B., Solinsky K.A., Desilva U. Diaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D., Sagripanti J.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: Receptor for the MCP-1, MCP-3 and MCP-4 chemokines. Transduces a signal by increasing the intracellular calcium ions level. Alternative coreceptor with CD4 for HIV-1 infection. SUBCELLULAR LOCATION: Integral membrane protein.
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SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SECURNCE FROM N.A., AND VARIANTS ILE.64 AND GLU-355.
Rieder M.J., Armel T.Z., Carrington D.P., Ozuna M., Kuldanek S.A.,
Rajkumar N., Toth B.J., Yi Q., Nickerson D.A.;
"SeattleSNPs. NHIBI HI66682 program for genomic applications, UW-FHCRC, Seattle, WA (URL: http://pga.gs.washington.edu).";
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
Yamagami S., Tokuda Y., Ishii K., Tamaka H., Endo N.; "cDNA cloning and functional expression of a human monocyte chemoattractant protein 1 receptor."; Biochem. Biophys. Res. Commun. 202:1156-1162(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bold=P41597-2; Sequence=VSP_001893;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IsoId=P41597-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Immunol. 165:5295-5303(2000)
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PIR; 138450; 138450.
PIR; JC2443; JC2443.
PDB; IKAD; Model; A=1-349.
PDB; IKPI; Model; A=1-349.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               U80924; AACS1636.1; -. U95626; AAB57791.1; -.
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MIM; 601267; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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RGD; 620876;
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                                (sensu Verte. . .; TAS
                                                                                     . .; TAS
                                                                                                                                                                                                                                                                                                                                          By similarity.
SLFHIALGCRIAPLQXPVCGGPGVRPGKNVKVTTQGLLDGR
GKGKSIGRAPEASLQDKEGA -> RYLSVFFRKHITKRFCK
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GO:0005887; C:integral to plasma membrane; TAS.
GO:0005625; C:soluble fraction; TAS.
GO:0004950; F:chemokine receptor activity; TAS.
GO:0019735; P:actimicrobial humoral response (sensu Verte...)
GO:000598; P:chemotaxis; TAS.
GO:0007204; P:cytosolic calcium ion concentration elevation;
GO:0006954; P:intlammatory response; TAS.
GO:0007259; P:JAK-STAT cascade; TAS.
GO:0007194; P:negative regulation of adenylate cyclase ac...
                                                                                                                                PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
3D-structure; Alterative splicing; G-protein coupled receptor; Glycoprotein; Polymorphism; Sulfation; Transmembrane.
                                                                                                                                                                                                                                                                                                      7 (Potential).
Cytoplasmic (Potential).
N-linked (GlcNAc. . .) (Potential).
Sulfotyrosine.
                                                                                                                                                                                                                                                                                                                                                                       QCPVFYRETVDGVTSTNTPSTGEQEVSAGL (in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1651.5; DB 1; Length 374;
                                                                                                                                                                                                                  3 (Potential).
Cytoplasmic (Potential).
4 (Potential).
Extracellular (Potential).
5 (Potential)
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                                                                                                                                                                                                                                                                                   6 (Potential).
Extracellular (Potential).
                                                                                                                                                                               Extracellular (Potential).
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V -> I (in dbSNP:1799864).
/FTId=VAR_014339.
                                                                                                                                                                                                 Cytoplasmic (Potential).
2 (Potential).
Extracellular (Potential).
3 (Potential).
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                                                                                                                                                                                                                                                                      Pred. No. 4.2e-94;
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                                                                                                                                                                                                                                                                                                                                                                                                                       3 -> E.
/FTId=VAR 014340.
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                                                                                                                                                                                          (Potential)
                                                                                                                                                                                                                                                                            Cytoplasmic
                                                                                          InterPro; IPR002237; CC 2 receptor.
InterPro; IPR000355; Chmkine receptor.
InterPro; IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                                                                                                                                 (Boform B)
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                                                                                                                        Pfam; PF00001; 7tm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
C-C chemokine receptor type 2 (C-C CKR-2) (CC-CKR-2) (CCR-2).
Name=CCr2; Synonyms=Cmkbr2;
                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

    macrophages.
    INDUCTION: In animals in which experimental allergic encephalomyelitis (EAE) has been induced.
    SIMILARITY: Belongs to the G-protein coupled receptor 1 family.

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Potential.
Extracellular (Potential)
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Potential.
Extracellular (Potential)
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Cytoplasmic (Potential).
301 NPIIYAFVGEKFR---SLF---HIALG-CRIAPL 327
                                                                                                                                               373 AA
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PROSITE; PR00237; G PROTEIN RECEP F1 1; 1.

PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.

G-protein coupled receptor; Transmembrane.

DOMAIN

61 81 Potential
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InterPro; IPR000276; GPCR_Rhodpsn.
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                                                                                                                                               STANDARD;
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126
373 AA;
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81.2%; Score 1542; DB 1; Length 373;

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                                                                                                                                                                                                                                                                                                                                                                            121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
                                                                                                                                                                                                                              AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
                                                                                                                                                                                                                                                                                                                                                                                                                                             73
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MEDLINE=97026720; PubMed=8872898;

MEDLINE=97026720; PubMed=8872898;

DOI=10.1002/(SICI)1097-4547(19960815)45:4<382::AID-JNR7>3.3.CO;2-H;

DOI=10.1002/(SICI)1097-4547(19960815)45:4<382::AID-JNR7>3.3.CO;2-H;

DOI=10.1002/(SICI)1097-4547(19960815)45:4<382::AID-JNR7>3.3.CO;2-H;

POST T.W., Gerard C., Dorf M.E.;

"MOUSE astrocytes respond to the chemokines MCP-1 and KC, but reverse transcriptase-polymerase chain reaction does not detect mRNA for the transcriptase-polymerase chain reaction does not detect mRNA for the transcriptase-polymerase chain reaction does not detect mRNA for the transcriptase. J. Neurosci. Res. 45:382.391(1996).

J. Neurosci. Res. 45:382.391(1996).

-i- FUNCTION: Receptor for the MCP-1 (JE), MCP-3 (FIC) and MCP-5 chemokines. Transduces a signal by increasing the intracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chemoattractant protein 1) and murine macrophage inflammatory protein lalpha receptors: evidence for two closely linked C-C chemokine
                                                                                    14 ILSTSHSLFPRSIQELDEGATTPYDYDDGEPCHKTSVKQIGAWILPPLYSLVFIFGFVGN
                                                               1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN
                                                                                                                                    MLVVLILINCKKCKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Molecular cloning and functional expression of murine JE (monocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=96205938; PubMed=8631787; DOI=10.1074/jbc.271.13.7551;
Boring L., Gosling J., Monteclaro F.S., Lusis A.J., Tsou C.-L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=BALB/C;
MEDLINE=96216064; PubMed=8662823; DOI=10.1074/jbc.271.20.11603;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P51683; Q61172;
01-OCT-1996 (Rel. 34, Created)
01-NOY-1997 (Rel. 35, Last sequence update)
C-CT-2004 (Rel. 45, Last annotation update)
C-C chemokine receptor type 2 (C-C CKR-2) (CC-CKR-2)
(JE/FIC receptor) (MCP-1 receptor).
                             48; Indels
              2.3e-87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          373 AA
             Pred. No. 2.3e; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biol. Chem. 271:7551-7558(1996)
80.0%; #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       receptors on chromosome 9
                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                 288;
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                                 Matches
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133
                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 MLVVLILINCKKLKCLTDIYLLNIAISDILFLITLPLWAHSAANEWVFGNAMCKLFTGLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74 MLVIIILIGCKKLKSMTDIYLLNLAISDLLFLLTLPFWAHYAANEWVFGNIMCKVFTGLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK
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                                                                                                                                                                                                                                        MGD; MG1:106185; CCT2.

G0; G0:0016493; F:C-C chemokine receptor activity; IDA.

G0; G0:0016493; F:C-C chemokine receptor activity; IDA.

G0; G0:001606; P:C-C chemokine response (sensu Vertebrata); IMP.

G0; G0:001606; P:C-C chemokina response; IMP.

G0; G0:0016959; P:hemopoiesis; IMP.

G0; G0:000659; P:inflammarory response; IMP.

G0; G0:0019233; P:perception of pain; IMP.

G0; G0:0019233; P:perception of cell migration; IMP.

InterPro; IPR0002237; C2 receptor.

InterPro; IPR000255; Chmkine receptor.

InterPro; IPR000276; GPCR_Rhodpsn.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- TISSUE SPECIFICITY: Detected in monocyte/macrophage cell lines,
but not in nonhematopoietic cell lines.
-!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cytoplasmic (Potential).

Cytoplasmic (Potential).

2 (Potential).

Stracellular (Potential).

3 (Potential).

Cytoplasmic (Potential).

4 (Potential).

Cytoplasmic (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 (Potential).
Cytoplasmic (Potential).
By similarity.
Y -> H !:-
                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00001; Trm 1; J. PRINTS; PR0001; Trm 1; J. PRINTS; PR000237; GPCRRHODPSN. PROSITE; PS00237; G PROTEIN RECEP_F1_1; 1. PROSITE; PSS0262; G PROTEIN RECEP_F1_2; 1. PROSITE; PSS0262; G PROTEIN RECEP_F1_2; 1. DOMAIN COUPLE of Feceptor; Transmembrane. DOMAIN 1 5.5 Extracellular (Potential). TRANSMEM 56 83 1 (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42782 MW; FA012C10F4C9325A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Y -> H (in Ref. 1)
A -> G (in Ref. 1)
V -> G (in Ref. 1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25; Mismatches
                                                                                                                                                                                                EMBL; U47035; AAC52453.1; -. EMBL; U51717; AAC52557.1; -.
                                                                                                                                                                                                                  U56819; AAC52557.1; -. U56819; AAC52784.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       287; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83
93
1114
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239
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373 AA;
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TRANSMEM
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TRANSMEM
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TRANSMEM
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181 COKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240
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InterPro; IPR002240; CC_5 receptor.
InterPro; IPR000355; Chmkine receptor.
InterPro; IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam, PF00001, 7tm i, 1.
PRINTS, PR00657, CCCHEMOKINER.
PRINTS, PR01110, CHEMOKINERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73.8%;
                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Director MGC Project;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mouse cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=Cmkbr5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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EMBL; AP006435; BAD08655.1; -.

EMBL; AP019271; BAD12134.1; -.

R GO; GO: 0016021; C:integral to membrane; IRA.

GO; GO: 0016021; C:integral to membrane; IRA.

GO; GO: 0016932; F:receptor activity; IRA.

GO; GO: 001884; F:rhodopsin-like receptor activity; IRA.

GO; GO: 001886; P:rhodopsin-like receptor activity; IRA.

R GO; GO: 001886; P:rhodopsin-like receptor protein signalin. . .; IRA.

InterPro; IPR00235; Chmkine receptor.

InterPro; IPR00355; Chmkine receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                             MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
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                AVRVIFTIMIVYFLFWTPYNIVILLANTFORFFGLSNCESTSOLDOATOVTETLGMTHCCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shinkai H., Morozumi T., Toki D., Muneta Y., Awata T., Uenishi H.; Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Uenishi H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sus scrofa (Pig).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Suina; Suidae; Sus.
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                                                                                                                                                                                                                                                                                                      05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Chemokine (C-C motif) receptor 2 (Chemokine C-C motif receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shinkai H., Morozumi T., Toki D., Muneta Y., Awata T., I
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       373 AA; 42299 MW; FABE55CA527A34E0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1513; DB 2;
Pred. No. 1.4e-85;
                                                                                                                                                                                                                                                                 373 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28; Mismatches
                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00657; CCCHEMOKINER.
PRINTS; PR01107; CHEMOKINER2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00237; GPCRRHODOPSN
                                                                                                                                                                                                                                                                                                    (TrEMBLrel. 27, C
(TrEMBLrel. 27, L
(TrEMBLrel. 27, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79.6%;
78.9%;
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                                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                      Name=CCR2;
                                                       254
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Q6YT42;
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R. T. Subendaniusy;

R. T. Subendaniusy;

R. Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

R. Attausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

R. Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

R. Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

R. Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

R. Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

R. Brachenco M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

R. Brownstein M.J., Usdin T.B., Toshiyuki S., Carrinci P., Prange C.,

R. Bosak S.A., McKwam P.J., McKernan K.J., Abramson R.D., Mullahy S.J.,

R. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

R. Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

R. Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

R. Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

R. Richwelsey R.W., Touchman J.W., Green E.D., Dickson M.C.,

R. Richmer A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

R. Montes S.J., Marra M.A.,

Jones S.J., Marra M.A.,

R. Grimman H., Green E.D., Schnerch A., Schnein J.E.,

R. Grimman A., Smailus D.E., Schnerch A., Schnein J.E.,

R. Grimman A., Smailus D.E., Schnerch A., Schnein J.E.,

R. Grimman A., Smailus D.E., Schnerch A., Schnein J.E.,

R. Grimman A., Smailus O, More C.,

R. Grimman A., Smailus O, More C.,

R. Grimman D. W., Smailus O, Wolley R.M., Butterfield Y.S.,

R. Grimman A., Smailus O, More C.,

R. Grimman D. W., Smailus O, More C.,

R. Grimman D. W., Smailus O, More C.,

R. Grimman D. W., Smailus O, Wolley R.M., Schnein J.E.,

R. Grimman D. W., Smailus O, Wolley R.M., Schnein J.E.,

R. Grimman D. W., Smailus O, Wolley R.M., Schnein J.E.,

R. Grimman D. W., Smailus O, Wolley R.M., Schnein J.E.,

R. Grimman D. W., Smailus O, Wolley R.M., Schnein J.E.,

R. Grimman D. W., Smailus O, Wolley R.M., Schnein J.E.,

R. Grimman D. W., Smailus O, Wolley R.M., Schnein J.E.,

R. Grimman D. W., Smailus C., 
                                                                                                                                                                                                                                                                                                                                                                                                                     301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     314 NPIIYAFVGEKFRRYLSVFFRKHIAKHLCKQCPVFYGETGDRMSSTYTPSTGEQEVSAAL 373
241 AVRVIPTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI
                                                                                                                                                                                                                                              254 AVRLIEVIMIVYFLFWAPYNIVLLISTFQVFFGLSNCKNSSQLDQAMQVTETLGLTHCCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rarium jorvegicus (Rat).
Ebkaryota: Merazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattua.
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EMBL; BC078756; AAH78756.1; -
GO; GO:0004872; F:receptor activity; IEA.
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Chemokine (C-C) receptor 5.
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PROSITE; PS00196; COPPER BLUE; UNKNOWN 1.
PROSITE; PS00237; G PROTEIN RECEP F1 1; UNKNOWN 1.
PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
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Pred. No. 7.7e-79;
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Virol. 71:8642-8656(1997)
                        SEQUENCE FROM N.A.
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                                                                                   SMTDIYLFNLAISDLLFLTLDFWAHYAANEWVFGNIMCKLFTGIYHIGYFGGIFFIILL 124
                                                                                                                    135 TIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCOKEDSVYVCGPYF 194
                                                                                                                                                                  P----RGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNBKKRHRAVRVIFTIMI 250
                                                                                                                                                                               245 VYFLFWTPYNIVLLTTTFQEYFGINNCSSSNRLDQAMQVTBTLGWTHCCLNPVIYAFVGB 304
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                                           GSIPTYIYDIDYSMSAPCQKFNVKQIAAQLLPPLYSLVFIFGFVGNNMVFLILISCKKLK 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chemoattractant protein 1) and murine macrophage inflammatory protein lalpha receptors: evidence for two closely linked C-C chemokine receptors on chromosome 9.";
                          17 GEEVITTPFDYDY--GAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLK
                                                                        75 CLIDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILL
    6; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [4] SEQUENCE FROM N.A.
STRAIN=CS7BL/6, and NIH Swiss; TISSUE=Kidney, Liver, and Spleen;
STRAIN=S98001387; PubMed=9343222;
Kuhmann S.E., Platt E.J., Kozak S.L., Kabat D.;
Kuhmann G.E., platt E.J., Kozak S.L., Kabat D.;
implymorphisms in the CCR5 genes of African green monkeys and mice implicate specific amino acids in infections by simian and human immunodeficiency viruses.";
                                                                                                                                                                                                                                                                                                                                                                                                      (MIP-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=C57BL/6 X CBA; TISSUE=Thymus;
STRAIN=C57BL/6 X CBA; TISSUE=Thymus;
MEDLINE=96278910; PubMed=8662890; DOI=10.1074/jbc.271.24.14445;
MEDLINE=96278910; PubMed=8662890; DOI=10.1074/jbc.271.24.14445;
Meyer A., Coyle A.J., Proudfoot A.E.I., Wells T.N.C., Power C.A.;
"Cloning and characterization of a novel murine macrophage
inflammatory protein-1 alpha receptor.";
J. Biol. Chem. 271:14445-14451(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRANN=129/SvJ, TISSUE-Spleen;
MEDLINE=96205938; Pubmed=8631787; DOI=10.1074/jbc.271.13.7551;
BOTING L., Gosling J., Monteclaro F.S., Lusis A.J., Tsou C.-L.,
                                                                                                                                                                                                                                                              311 KFRRYLSVPFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL 360
                                                                                                                                                                                                                                                                                                                                         CRES MOUSE STANDARD; PRT; 354 AA.
P51682; 035313; 035891; P97308; P97405; Q61867;
01-0CT-1996 (Rel. 34, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
25-OCT-2090 (Rel. 45, Last annotation update)
C-C chemokine receptor type 5 (C-C CRR-5) (CCR-5)
                                                                                                                                                                                                                                                                          50; Indels
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Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
    30; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                 alpha receptor).
Name=Ccr5; Synonyms=Cmkbr5;
Mus musculus (Mouse).
       Conservative
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00001; 7cm 1; PF0000N.
PRINTS; PR00237; G_CRAPBIO RECEP F1 1; 1.
PROSITE; PS00237; G_PROTEIN RECEP F1 2; 1.
PROSITE; PS50262; G_PROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Glycoprofein; Polymorphism; Transmembrane.
                                                                                                                                    MEDILINE=97404635; PubMed=9261347;
Doranz B.J., Lu Z.H., Rucker J., Zhang T.Y., Sharron M., Cen Y.H.,
Doranz B.J., Lu Z.H., Rucker J., Zhang T.Y., Sharron M., Cen Y.H.,
Wang Z.X., Guo H.H., Du J.G., Accavitti M.A., Doms R.W., Peiper S.(
"Two distinct CCR5 domains can mediate coreceptor usage by human
immunodeficiency virus type 1.";
J. Virol. 71:6305-6314(1997).
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2 (Potential).
Extracellular (Potential)
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Cytoplasmic (Potential).
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EMBL, AAC1977.2, AAB71183.1; --
EMBL, D93648; BAA12024.1; --
MGD; MGI:107182; Ccr5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, U47036; AAC52454.1; -. EMBL, X94151; CAA63867.1; -. EMBL; U68565; AAB37273.1; -. EMBL; U83327; AAC53386.1; -.
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SEQUENCE FROM N.A.
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Zhang Y., Ryder O.A., Zhang Y.;

Zhang Y., Ryder O.A., Zhang Y.;

Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.

-!- SUBJELLULAR LOCATION: Integral membrane protein (By similarity)

-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

EMBL, ARITYS87, AR443370.1;

GO, GO:0016021; C:integral to membrane; IEA.

GO, GO:0016493; F.C-C chemokine receptor activity; IEA.

GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

GO, GO:0001186; P:rhodopsin-like receptor activity; IEA.

GO; GO:0001186; P:G-protein coupled receptor protein signalin. .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Platyrrhini, Cebidae, Callicebinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          KFRRYLSVFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL 360
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                                                                                                                                     Length 354;
                                                                                                                                                              50; Indels
                                                                                                        B4A6B942E88F9CF0 CRC64;
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Last annotation update)
I -> V.

I -> M.

F -> L (in Ref. 2).

L -> F (in Ref. 2).

N -> I (in Ref. 3).

P -> S (in Ref. 3).
                                                                                                                                  73.5%; Score 1396; DB 1;
74.6%; Pred. No. 2.1e-78;
iive 33; Mismatches 50;
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GO; GO:0001884; F:rhodopsin-like recep
GO; GO:0007186; P:C-protein coupled re
InterPro; IPR00923; BlueCu I
InterPro; IPR000240; CC 5 receptor.
InterPro; IPR000355; Chmkine receptor.
InterPro; IPR000276; GPCR_Rhodpsn.
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Callicebus moloch (Dusky titi).
                                                                                                         40863 MW;
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PRINTS; PR00657; CCCHEMOKINER,
PRINTS; PR01110; CHEMOKINERS.
PRINTS; PR00237; GPCRRHODOPSN.
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                                                                                                                                                            Matches 261; Conservative
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208
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318
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MEDLINE=Sprague-Dawley;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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25-OCT-2004 (Rel. 45, Last annotation update)
C-C chemokine receptor type 5 (C-C CRR-5) (CC-CKR-5) (MIP-1
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MEDININE-98334064; PubMed=9670989;
DOI=10.1002/(SICI)1097-4547(19980701)53:1<16::AID-JNR3>3.3.CO;2-0;
BOI=10.1002/(SICI)1097-4547(19980701)53:1<16::AID-JNR3>3.3.CO;2-0;
Boliss O., Gourmala N., Boddeke H.W.G.M., Sauter A., Fiebich B.L.,
Berger M., Gebicke-Haerter P.J.;
"Cloning Of rat HIV-1-chemokine coreceptor CKR5 from microglia and upregulation of its mRNA in ischemic and endotoxinemic rat brain.";
J. Neurosci. Res. 53:16-28(1998).
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PROSITE; PS00196; COPPER BLUE; UNKNOWN 1.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Receptor; Transmembrane.
SEQUENCE 352 AA; 40495 MW; 7FB307513ACF9B9B CRC64;
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Query Match
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                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          185 LHIQYRFWKHFQTLKAVILSLILPLLVAVICYSGIIANTLFRCRNEKKRHRAVRLIFAIMI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               135 TIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCOKEDSVYVCGPYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   195 ---- PRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 GEEVITIFDYDY -- CAPCHKFDVKOIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLK
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N-linked (GlcNAc. . .) (Potential)
77EDB368AA4C868D CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (Potential).
Cytoplasmic (Potential).
Extracellular (Potential).
3 (Potential).
Cytoplasmic (Potential).
Extracellular (Potential).
Extracellular (Potential).
5 (Potential).
Cytoplasmic (Potential).
6 (Potential).
6 (Potential).
Extracellular (Potential).
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PROSITE; PS00237; GPROTEIN RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN RECEP_F1_2; 1.
G_PROTEIN RECEP_F1_2; 1.
G_PROTEIN RECEP_F1_2; 1.
TRANSMEM 33 60 1 (Potential).
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InterPro; IPR002240; CC 5 receptor.
InterPro; IPR00355; Chmkine_receptor.
InterPro; IPR00276; GPCR_Rhodpsn.
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352 AA.

Q6YT41; 05-JUL-2004 (TrEMBLrel. 27, Created)

Q6YT41

RESULT 10 QEYT41 ID QEYT4: AC QEYT4: DT 05-JU

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136 IDRYLAIVHAVPALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFP 195
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EMBL; AB11927; BAD12135.1; -.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0016493; P:C-C chemokine receptor activity; IEA.
GO; GO:004842; P:receptor activity; IEA.
GO; GO:0004841; P:receptor activity; IEA.
GO; GO:0001584; P:rhodopsin-like receptor activity; IEA.
GO; GO:0001186; P:G-protein coupled receptor protein signalin. .; IEA.
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                                                                                                                                                                                                                                                                                                           T., Toki D., Muneta Y., Awata T., Uenishi H.;
to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                       Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Suina, Suidae, Sus.
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to the EMBL/GenBank/DDBJ databases.
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Chemokine (C-C motif) receptor 5 (Chemokine C-C motif eceptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
Shinkai H., Morozumi T., Toki D., Eguchi T., Muneta Y., Awata
Uenishi H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72.8%; Score 1383; DB 2; Length 352; 74.5%; Pred. No. 1.3e-77; ive 33; Mismatches 50; Indels
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PROSITE; PS0137; G PROTEIN RECEP F1 1; 1.
PROSITE; PS01262; G PROTEIN RECEP F1 2; 1.
GPOTE PS01262; G PROTEIN RECEP F1 2; 1.
SEQUENCE 352 AA; 40227 MW; 7464CB930911C987 CRC64;
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Interpro; IPR002240; Cc_5 receptor.
Interpro; IPR00025; Chmkine_receptor.
Interpro; IPR000276; GPCR_Rhodpsn.
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PRINTS; PR00657; CCCHEMOKINER.
PRINTS; PR01110; CHEMOKINERS.
PRINTS; PR00237; GPCRRHODOPSN.
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                                                                                                                                                                                                                                                                                                                     Submitted (JAN-2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                            Shinkai H., Morozumi
Submitted (MAY-2003)
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                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                Sus scrofa (Pig)
                                                                                                                                                                                                              NCBI_TaxID=9823;
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                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

Soares E.A.J.M., Schrago C.G., Ribeiro I.P., Pissinatti A.,

Soares E.A.J.M., Schrago C.G., Ribeiro I.P., Pissinatti A.,

Soares E.A.J.M., Schrago C.G., Ribeiro I.P., Pissinatti A.,

Sequence H.A., Russo C.A.M., Tanuri A., Soares M.A.,

Sequence H.A., Russo C.A.M., Tanuri A., Soares M.A.,

Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.

C. -- SIMIAMITY: Belongs to family 1 of G-protein coupled receptors.

EMBL; AV278747; AAQ20015.1; -- membrane; IEA.

BR GO; GO:0016021; C:integral to membrane; IEA.

BR GO; GO:0016872; P:receptor activity; IEA.

GO; GO:0001884; P:receptor.

InterPro; IPR0002240; C.S. Feceptor.

InterPro; IPR0002240; C.S. Feceptor.

InterPro; IPR000235; ChmkIne_receptor.

InterPro; IPR000215; ChmkIne_receptor.

BR FRINTS; PR001110; HEMBOKINER.

PROSITE; PS00196; COPPER BLUE; UNKNOWN_1.

PROSITE; PS00196; COPPER BLUE; UNKNOWN_1.

PROSITE; PS00196; COPPER BLUE; Transmembrane.

SP PROSITE; PS00237; GPROTEIN RECEP P1_2; 1.

ROSITE; PS002262; GPROTEIN RECEP P1_2; 1.

ROSITE; PS00237; GPROTEIN RECEP P1_2; 1.

ROSITE; PROSITE; PROTEIN RECEP P1_2; 1.

ROSITE; PROSITE; PROTEIN RECEP P1_2; 1.

ROSITE; PS00237; GPROTEIN RECEP P1_2; 1.

ROSITE; PROTEIN RECEP P1_2; 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            258 PYNIVILLNTPQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRYLS 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         142 IVHAVPALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG---- 197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gapa
                                                                                                                                                                                                Leontopithecus chrysopygus (Gold-and-black lion tamarin).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Platyrrhini, Callitrichidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72.5%; Score 1377; DB 2; Length 352; 75.2%; Pred. No. 3e-77; ive 32; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     318 VFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL 360
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                                                                               05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                            352 AA
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                                       PRELIMINARY;
                                                                                                                                                        CC chemokine receptor 5.
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                                                                                                                                                                                                                                                                                           NCBI_TaxID=58710;
                                                                                                                                                                                                                                                                      Leontopithecus
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nes 258;
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RESULT 12 CKR5_CERTO

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@ib.ch).
                                                                                                                                                                                                                               STRAIN-085, 087, 089, and Isolate 079;

MEDLINE-98321155; PubMed=9656999; DOI=10.1006/viro.1998.9174;

MEDLINE-98321155; PubMed=9656999; DOI=10.1006/viro.1998.9174;

MEDLINE-98321155; PubMed=9656999; DOI=10.1006/viro.1998.9174;

Perimary SIVBM isolates use the CCR5 coreceptor from sooty mangabeys naturally infected in west Africa: a comparison of coreceptor usage of primary SIVBM, HIV-2, and SIVBMc.";

Virology 246:113-124(1998)

-!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha, MIP-1-beta and RANTES and subsequently transduces a signal by increasing the intracellular calcium ions level. May play a role in the control of granulocytic lineage proliferation or
          062743; 062744; 062745; 062746; 15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last amortation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
Name=CCR5, Synonyma=CMKBRS;
Cercocebus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00217; GPCRHODOPSN.
PROSITE; PS00237; G PROTEIN RECEP_F1 1; 1.
PROSITE; PS50262; G PROTEIN RECEP_F1 2; 1.
G-protein coupled receptor; Glycoprotein; Sulfation; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                          differentiation.
-!- SUBCELULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bý similarity.
Sulfotyrosine (By similarity)
Sulfotyrosine (By similarity)
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Sulfotyrosine (By similarity)
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Cytoplasmic (Potential).
2 (Potential).
Extracellular (Potential)
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Cytoplasmic (Potential).
4 (Potential).
Extracellular (Potential)
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6 (Potential).
Extracellular (Potential)
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-> D (in isolate 079).
-> G (in isolate 087).
-> K (in isolate 079).
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EMBL; AF051903; AAC39831.1; -.
EMBL; AF051904; AAC39832.1; -.
EMBL; AF051905; AAC39833.1; -.
InterPro; IPR002240; CC 5 receptor
InterPro; IPR003055; ClmkIne receptor
InterPro; IPR0030576; GPCR_Rhodpsn.
Pfam; PP00001; 7tm_1; 1.
                                                                                                                                                                   Cercopithecinae; Cercocebus
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688
1102
1124
1124
1136
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                                                                                                                                                                                   NCBI_TaxID=9531;
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us-10-791-166-4.rup

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Cercopithecinae; Cercocebus.
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REQUENCE FROM N.A.

RECURDE-2156835; PubMed=11711592;

REDIATE-2156835; PubMed=11711592;

RECLAINE-2156835; PubMed=11711592;

RECLAINE-2156835; PubMed=11711592;

RECLAINE B.T., Kaiken C.L., Tooze Z., Goeken R.M., Brown C.R., Husch V.M.;

RECLAIR M., Korber B.T., Hirsch V.M.;

R. Capped mangabeys from Nigeria (SIVzcmNG409 and -NG411).";

T. Virol. 75:12014-12027(2001).

T. Virol. 75:12014-12027(2001).

RECLAIR M. AF349682; AAK69684.1; -...

SEMBL; AF349682; AAK69684.1; -...

REDIATE AF349682; ARK69684.1; -...

REDIATE AF349682; Fireceptor activity; IEA.

ROG GO:0016021; C:integral to membrane; IEA.

ROG GO:0016021; C:integral to membrane; IEA.

ROG GO:0016021; C:integral to membrane; IEA.

ROG GO:0016031; C:integral to membrane; IEA.

ROG GO:0016031; C:integral to membrane; IEA.

ROG GO:0016032; C:integral to membrane; IEA.

ROG GO:0016035; C:integral to membrane; IEA.

ROG GO:0016036; C:integral to membrane; IEA.

ROG GO:0016036; C:integral to membrane; I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         142 IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFP----RG 197
                                                                                                                                                                                                                                                                                                                                                                       INLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLA 141
                                                                                                                                                                                                                                                                                              WINIPHTIMRNILGLVLPLLIMVICYSGILKTILLRCRNEKKRHRAVRVIFTIMIVYFLFWT
                                                                                                                                                                                                                                                             24 FDYDY -- GAPCHKFDVKQIGAQLLPPLYSLVPIFGFVGNMLVVLILINCKKLKCLTDIYL
107 L -> V (in isolate 089).

134 V -> G (in isolate 079).

146 V -> L (in isolate 085 and isolate 089).

340 T -> I (in isolate 079).

40489 MW, 20A196E2D47E49CA CRC64;
                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Cercocebus.
MCBI_TaxID=81944;
                                                                                                                                                                                                               9
                                                                                                                                                     72.4%; Score 1376; DB 1; Length 352; 76.4%; Pred. No. 3.5e-77; ive 31; Mismatches 44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           318 VFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-JUL_2004 (TrEMBLrel. 27, Created)
05-JUL_2004 (TrEMBLrel. 27, Last sequence update)
05-JUL_2004 (TrEMBLrel. 27, Last annotation update)
Chemokine receptor CCR5.
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PRINTS; PR01110; CHEMOKINERS.
PRINTS; PR00237; GPCRRHODOPEN.
                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
     107
134
146
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352 AA;
                                                                                                                                                                                         Similarity
                                                                                                                                                                                            Best Local Sim
Matches 262;
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                                                                                    VARIANT
SEQUENCE
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                                                                                                                                                                   Query Match
     VARIANT
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EQUENCE FROM N.A.

MEDLINE=99059829; PubMed=9841919;
Achen Z., Kwon D., Jin Z., Monard S., Telfer P., Jones M.S., Lu C.Y.,
Aguilar R.P., Ho D.D., Marx P.A.,
In artural infection of a homozygous delta24 CCRS red-capped mangabey
if with an R2D-tropic simian immunodeficiency virus.";
with an R2D-tropic simian immunodeficiency virus.";
IL Exp. Med. 188:2057-2055(1998)
IL SUBCELULAR LOCATION: Integral membrane protein (By similarity).
IL SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
EMBL; AF084004; AAC62472.1;
CO: 00:0016021; C:integral to membrane; IEA.
CO: GO: 00:004872; F: receptor activity; IEA.
CO: GO: 00:004872; F: receptor activity; IEA.
CO: GO: 00:00186; P: Prodopsin-like receptor activity; IEA.
CO: GO: 00:00186; P: Prodopsin-like receptor activity; IEA.
CO: GO: 00:000186; P: Richodopsin-like receptor activity; IEA.
CO: GO: 00:000186; P: Richodopsin-like receptor protein signalin. ..; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 257
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae,
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                                                                                                                                                            Length 352;
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PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Receptor; Transmembrane.
SEQUENCE 352 AA; 40489 MW; 20A196E2D47E49CA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NAV-2004 (TrEMBLrel. 26, Last annotation update)
Chemokine receptor CCR5.
                                                                                                                                                                   DB 2;
                                                                                                                                                            Query Match 72.4%; Score 1376; DB 2;
Best Local Similarity 76.4%; Pred. No. 3.5e-77;
Matches 262; Conservative 31; Mismatches 44
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PRINTS; PR00657; CCCHEMOKINER.

PRINTS; PR0110; CHEMOKINERS.

PRINTS; PR00237; GPCRHODOPSN.

PROSITE; PS00237; GPCRHODOPSN.

PROSITE; PS50262; GPROTEIN_RECEP_F1_1; 1.

PROSITE; PS50262; GPROTEIN_RECEP_F1_2; 1.
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InterPro; IPR000355; ChmkIne receptor.
InterPro; IPR000276; GPCR_Rhodpsn.
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1. SIMILARITY: Belongs to family 1 of G-protein (By similarity).

2. I. SIMILARITY: Belongs to family 1 of G-protein (By similarity).

2. I. SIMILARITY: Belongs to family 1 of G-protein (By similarity).

2. I. SIMILARITY: Belongs to family 1 of G-protein (By similarity).

3. EMBL; AV278742; AAQ2010.1; -

3. EMBL; AV278742; AAQ2010.1; -

3. EMBL; AV278742; AAQ2010.1; -

3. Exceptor activity; IEA.

4. GO; GO:000186; P:G-protein coupled receptor protein signalin. .; IEA.

5. GO:000186; P:G-protein coupled receptor protein signalin. .; IEA.

6. GO:000186; P:G-protein coupled receptor protein signalin. .; IEA.

7. InterPro; IPR000236; ChmkIne receptor.

8. InterPro; IPR000355; ChmkIne receptor.

8. InterPro; IPR000355; ChmkIne receptor.

8. RINTS; PR00001; 7tm 1; 1.

8. Pfam; PF00001; 7tm 1; 1.

8. RINTS; PR000110; CCCHEMOKINERS.
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Mammalia, Butheria, Primates, Platyrrhini, Cebidae, Cebinae, Saimiri
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MEDLINE=22174698; PubMed=12186836;
LaBonte J.A., Babcock G.J., Patel T., Sodroski J.;
LaBonted of HIV-1 infection of New World monkey cells occurs
primarily at the stage of virus entry.";
J. Exp. Med. 196:431-445(2002).
                                                      Length 352;
                                                  Query Match 72.4%; Score 1375; DB 2; Length 3
Best Local Similarity 76.1%; Pred. No. 4e-77;
Matches 261; Conservative 32; Mismatches 44; Indels
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Last sequence update)
Last annotation update)
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
05-ULL-2004 (TrEMBLrel. 27, Last annotation updat
Chemokine receptor CCR5 (CC chemokine receptor 5)
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PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00196; COPPER BLUE; UNKNOWN 1.
PROSITE; PS00237; G PROTEIN RECRP F1 1; 1.
PROSITE; PS50262; G PROTEIN RECRP F1 2; 1.
G-profein coupled receptor; Receptor; Transmembrane.
SEQUENCE 352 AA; 40542 MW; 9FC896FB7F074647 CRC64;
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Matches 360; Conservative
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              GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/08450393A

Sequence 4, Application US/08450393A

Patent No. 5707815

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT

TITLE OF INVENTION: ADMINESS:

MUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

MEDIUM TYPE: California

COUNTRY: USA

ZIP: 943-06-2155

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTION NOBER: US/08/450,393A

FILING DATE: MAY 25, 1995

CURSIPICATION NUMBER: US/08/450,393A

FILING DATE: MAY 25, 1995

CURSIPICATION NUMBER: UCAL-237/02US

TELEPAN: 415-643-5165

TELECOMMUNICATION INFORMATION:

MAWE: CSET', LUADN

MAWE: CSET', LUADN

MAWE: A15-643-5165

TELECOMMUNICATION INFORMATION:

MAWE: A15-687-0663

TELERA: 380816COOleyPA

MAPPLICATION OF SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 360 amino acide

TELENGTH: 360 amino acide
US-09-517-605-5
US-09-617-605-5
US-09-617-605-5
US-09-61-185-18
US-08-61-105-14
US-08-75-967A-2
US-08-77-56-5
US-09-796-202-1
US-09-938-719-5
US-09-939-226B-5
US-09-939-226B-5
US-09-939-226B-5
US-09-62-784A-2
US-09-502-784A-2
US-09-502-784A-2
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61 MLVVLILINCKKLKCLTDIYLLINLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
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REGISTRATION NUMBER: 36,207
REPRENCE/DOCKET NUMBER: MNI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)742-4414
INFORMATION FOR SEQ ID NO: 50: SEQUENCE CHARACTERISTICS:
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FRACMENT TYPE: internal
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US-09-045-583-50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Charo, Israel
APPLICANT: Coughlin, Shaun
TITLE OF INVENTION: PROTEIN RECEPTORS
INTER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
STREET: 5 Palo Alto Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,669
FILING DATE: MAY 25, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Neeley, Richard
REGISTRATION NUMBER: 30,092
REGISTRATION NUMBER: 30,092
RELECANONINICATION INFORMATION:
TELEPHONE: 415-843-5000
TELEPAX: 415-843-5000
TELEFAX: 380816CooleyPA
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 6132987
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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STATE: California
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US-U9-U45-S83-50

Sequence 50, Application US/09045583

Patent No. 6287805

GREERAL INFORMATION:
TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled NUMBER OF SEQUENCES: 56

CORRESPONDENCE ADDRESS: ADDRESSE: LAHIVE & COCKFIELD, LLP STREFT: 28 State Street
CITY: Boston STATE: ABSachusetts
COUNTRY: USA

ZIP: 02.109

COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: 1BW PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/09/045,583
FILING DATE: 20-MRR-98
CLASSIFICATION DATA:
APPLICATION NUMBER: RICHON NUMBER:
FILING DATE:
RELING                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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CCR2
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APPLICANT: O'Brien, Stephen J.
APPLICANT: Smith, Michael
APPLICANT: Carrington, Mary
TITLE OF INVENTION: DELAYED PROCRESSION TO ALE
TITLE OF INVENTION: MISSENSE ALLELE OF THE CEPTILE REPRENCE: 14014.0333
CURRENT APPLICATION NUMBER: US/09/131,827A
CURRENT PILING DATE: 1998-08-10
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/09131827A; Patent No. 6600030; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 360; Conserval
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LENGTH: 360
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IITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled
Heptahelical Receptor Superfamily and Uses
Therefor
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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100.0%; Pred. No. 8.6e-151;
ative 0; Mismatches 0;
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APPLICATION NUMBER: US/09/534,185
PILING DATE: 24-Mar-2000
CLASSIFICATION: cunknown>
PRIOR APPLICATION NUMBER: 09/045,583
FILING DATE: cunknown>
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REGISTRATION NUMBER: 36,207
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
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FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 50:
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 50, Application US/09534185
Patent No. 6403767
GENERAL INFORMATION:
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STATE: Massachusetts
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SEQUENCE CHARACTERISTICS:
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Best Local Similarity
Matches 360; Conserv
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                                                              Sequence 4, Application PC/TUS9500476
GENERAL INFORMATION:
APPLICANT: The Regents of the University of California TITLE OF INVENTION: MANMALIAN MONOCYTE CHEMOATTRACTANT TITLE OF INVENTION: PROTEIN RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Robbins, Berliner & Carson
                                                                                                                                                                                             ADDRESSE: Robbins, Berliner & Carson
STREET: 201 N. Figueroa Street, 5th Floor
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90012-2658
COMPUTER RADDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00476
FILING DATE:
CLASCYPET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INPORMATION:
NAME: Berliner, Robert
REGIESTRATION NUMBER: 20,121
REFRENCE/DOCKET NUMBER: 5555
TELECOMMUNICATION INPORMATION:
TELEPHONE: 310-977-1001
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amino acid
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Matches 360; Conservative
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US-09-949-016-11221
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                                                                                                                                                                                      NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSE: Cooley Godward Castro Huddleson & Tatum
STREET: 5 Palo Alto Square
              Sequence 4, Application US/09625573
Patent No. 6730301
GENERAL INFORMATION:
APPLICANT: Charo, Israel
COUGHLIA, Shaun
TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
PROTEIN RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Neeley, Richard
REGISTRATION NUMBER: 30,092
REFERENCE/DOCKET NUMBER: UCAL-237/01US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/625,573
FILING DATE: 25-U1-2000
CLASSIFICATION: CURROWN:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/446,669
FILING DATE: MAY 25, 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                        ZIP: 94306-2155
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 415-843-5000
TELEFAX: 415-857-0663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 360 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 380816CooleyPA
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                       CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
09-625-573-4
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Gaps

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; ORGANISM: Homo sapiens
US-09-131-827A-20
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ORGANISM: Homo sapiens
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US-09-826-509-473
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Sequence 11221, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: URDER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT FILING DATE: 2000-04-14

PRIOR PELLING DATE: 2000-04-14

PRIOR PELLING DATE: 2000-10-03

PRIOR PELLING DATE: 2000-10-03

PRIOR PELLING DATE: 2000-10-03

PRIOR PELLING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NOS: 207012

SEQ ID NOS: 207012

SEQ ID NOS: 207012
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         258 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCBSTSQLDQATQVTETLGMTHCCI 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN
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APPLICANT: O'Brien, Stephen J.
APPLICANT: Smith, Michael
APPLICANT: Smith, Michael
APPLICANT: Smith, Michael
APPLICANT: Smith, Michael
APPLICANT: Carrington, Mary
TITLE OF INVENTION: MISSENER ALIELE OF THE CCR2 GENE
FITE REPERRENCE: 14014.0333
CURRENT APPLICATION NUMBER: US/09/131,827A
CURRENT APPLICATION NUMBER: 60/055,659
PRIOR APPLICATION NUMBER: 60/055,659
PRIOR PILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 20, Application US/09131827A Patent No. 6600030 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JS-09-949-016-11221
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| Sequence 473, Application US/09826509 |
| Sequence 473, Application US/09826509 |
| Patent No. 6806054 |
| GENERAL INFORMATION: |
| APPLICANT: Lehmann-Bruinsma, Karin |
| APPLICANT: Liaw, Chen W. |
| TITLE OF INVENTION: No. 6806054-Endogenous, Constitutively Activated Known G |
| TITLE OF INVENTION: No. 6806054-Endogenous, Constitutively Activated Known G |
| TITLE OF INVENTION: Protein-Coupled Receptors |
| TITLE OF INVENTION: Protein-Coupled Receptors |
| TITLE OF INVENTION: Protein-Coupled Receptors |
| FILE REFERENCE: AREN-207 |
| CURRENT APPLICATION NUMBER: 60/195, 747 |
| PRIOR FILING DATE: 1998-10-13 |
| PRIOR FILING DATE: 1998-10-13 |
| NUMBER OF SEQ ID NOS: 589 |
| SOFTWARE: PatentIn Version 2.1 |
| LENGTH: 360 |
| LENGTH: 360 |
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                                                              Gaps
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Score 1899; DB 4; Length 360;
Pred. No. 1e-150;
1; Mismatches 0; Indels
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Pred. No. 2.7e-150;
0; Mismatches 1;
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   Query Match
Best Local Similarity 99.7%;
Matches 359; Conservative
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Best Local Similarity 99.7
Matches 359; Conservative
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FELEWIPYNIV 	pplication US/09938719 92938 92938 ANT SAMSON, MICHEL PARMENTIER, MARC VASSARI, GILBERT LIBERT, FREDERICK OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINE OF SEQUENCES: 17 PONDENCE ADDRESS: DDRESSEE Knobbe, Martens, Olson & Bear ITY: Newport Beach TATE: CA TATE: CA TATE: CA TOWNINY: U.S.A. IP: 92660 ER READABLE FORM: ER READABLE FORM: ER READABLE FORM: PPLICATION DATA: PPLICATION DATE: PLOPPY disk OMPUTER: IBM PC compatible PERATIOG SYSTEM: PC-DOS/MS-DOS OFTWARE: EA ang-2001 LING DATE: 24-ang-2001 LING DATE: 27-JULY-2000 EY/AGENT INFORMATION: CATABLE CATION NUMBER: 34,115 EFFERNCE/DOCKET NUMBER: 34,115 EFFERNCE/DOCKET NUMBER: 4,115 FOR SEQ ID NO: 7: FOR SEQ ID NO: 7: FOR SEQ ID NO: 7: ENGTH: 360 amino acide YER: amino acid FYPE: NO: 6692938e CE DESCRIPTION: SEQ ID NO: 7:	Query Match
QY 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240 Db 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240 CV 241 AVRVIFTIMIVYFLEWTPYNIVILLATFOBFFGLSNCESTSQLDQATQVTETLGWTHCCI 300 Db 241 AKRVIFTIMIVYFLEWTPYNIVILLATFOBFFGLSNCESTSQLDQATQVTETLGWTHCCI 300 CQY 301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPVFYRETVDGVTSTTNTPSTGEQEVSAGL 360 Db 301 NPIIYAFVGEKFRRYLSVFPRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL 360 Db 301 NPIIYAFVGEKFRRYLLSVFPRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL 360	33752 TR AND INACTIVE CC-CHE THEIC ACID MOLECULES THEIC ACID MOLECULES THEIC ACID MOLECULES THEIR AND INACTIVE IGH FLOOR THEIR THEIR THEIR THEIR THEIR THEIR THEIR THEIR THE	Best Local Similarity 98.3%; Pred. No. 1.5e-148; Matches 354; Conservative 2; Mismatches 4; Indels 0; Gaps 0; Qy 1 MLSTSRSPINTWESGESVTTFPYDYCAPCKPDVKOIGAOLLPPLYSLVFIFGFVGN 60 LI

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61 MLVVLILINCKKLKSLTDIYLLNLAISDLLFLITLFLWAHSAANEWVFGNAMCKLFTGLY 120
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                                          Sequence 51, Application US/09045583
Patent No. 6287805
GENERAL INFORMATION:
APPLICANT: Graham, Gerard J. et al.
TITLE OF INVENTION: No. 6287805e1 Molecules of the G Protein-Coupled NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/045,583
FILING DATE: 20-MAR-98
CLASSIFICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1849; DB 3;
Pred. No. 1.5e-146;
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REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MNI-044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
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Best Local Similarity 97.2%;
Matches 350; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 360 amino acids
amino acid
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                                                                                                                                                                                                                                                             CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
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APPLICANT: SAMSON, Michel.
APPLICANT: PARMENTIER, Marc
APPLICANT: VASSART, Gilbert
APPLICANT: LIBERT, Gilbert
APPLICANT: LIBERT, Frederick
TITLE OF INVENTION: Methods for Identifying Compounds which Bind the Active CCRS Chem
TITLE OF INVENTION: Receptor
FILE REFERENCE: 9409/2023C
FURENT APPLICATION NUMBER: US 09/939,226B
CURRENT PILING DATE: 2001-08-24
PRIOR PLILNG DATE: 1997-04-09
PRIOR PLILNG DATE: 1997-04-09
PRIOR APPLICATION NUMBER: US 09/626,939
PRIOR FILING DATE: 1997-04-09
PRIOR PLILNG DATE: 1997-04-09
PRIOR PLILNG DATE: 1997-03-04
NUMBER OF SEQ ID NOS: 18
SSOFIWARE: Patentin version 3.1
FURNIAND 1
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181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240
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                                               241 AVRVIFTIMIVYFLFWTPYNIVILLINTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI
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NAME/KEY: MISC_FEATURE
LOCATION: (325)..(327)
OTHER INFORMATION: Xaa = any amino acid
                                                                                                                                                                                                                                                                                                            Sequence 7, Application US/09939226B Patent No. 6800441 GENERAL INFORMATION:
APPLICANT: Euroscreen S.A.
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Best Local Similarity 98.3
Matches 354; Conservative
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US-09-939-226B-7
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Sequence 51, Application US/09534185
Patent No. 6403767
GENERAL INFORMATION:
APPLICANT: Graham, Gerard J. et al.
APPLICANT: Graham, Gerard J. et al.
TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled
Heptahelical Receptor Superfamily and Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 97.3%; Score 1849; DB 4;
Best Local Similarity 97.2%; Pred. No. 1.5e-146;
Matches 350; Conservative 5; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 09/045,583
FILING DATE: CUDACHOWN:
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
FERERCEGE DOCKET NUMBER: MNI-044
TELEPHONE: (617)227-7400
                                                                                                                                                                                                     NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESSE:
ADDRESSE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/534,185
FILING DATE: 24-Mar-2000
CLASSIFICATION: «UNKNOWN»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear

MOLECULE TYPE: peptide

FRAGMENT TYPE: internal

SEQUENCE DESCRIPTION: SEQ ID NO: 51:
US-09-534-185-51
                                                                                                                                                                             Therefor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                               CITY: Boston
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
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Search completed: June 9, 2005, 16:50:11 Job time : 30.9183 secs

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Sequence 460, App
Sequence 50, Appl
Sequence 64, Appl
Sequence 8, Appli
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Sequence 286, App
                                                                                                                                                                                                                                                    9, 2005, 16:48:19 ; Search time 100.545 Seconds (without alignments) 1372.524 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MLSTSRSRFIRNTNESGEEV......DGVTSTNTPSTGEQEVSAGL 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence (Sequence (Sequen
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1: /cgn2_6/ptodata/1/pubpaa/RCT TRW PUB.Popp:*

2: /cgn2_6/ptodata/1/pubpaa/RCT TRW PUB.Popp:*

4: /cgn2_6/ptodata/1/pubpaa/USO6_NEW PUB.pop:*

5: /cgn2_6/ptodata/1/pubpaa/USO6_NEW PUB.pop:*

5: /cgn2_6/ptodata/1/pubpaa/USO7_NEW PUB.pop:*

6: /cgn2_6/ptodata/1/pubpaa/USO8_NEW PUB.pop:*

7: /cgn2_6/ptodata/1/pubpaa/USO8_NEW PUB.pop:*

8: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pop:*

9: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pop:*

10: /cgn2_6/ptodata/1/pubpaa/USO9E_PUBCOMB.pop:*

11: /cgn2_6/ptodata/1/pubpaa/USO9E_PUBCOMB.pop:*

12: /cgn2_6/ptodata/1/pubpaa/USO9E_PUBCOMB.pop:*

13: /cgn2_6/ptodata/1/pubpaa/USO0B_PUBCOMB.pop:*

14: /cgn2_6/ptodata/1/pubpaa/USOOB_PUBCOMB.pop:*

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18: /cgn2_6/ptodata/1/pubpaa/USIOB_PUBCOMB.pop:*

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15: /cgn2_6/ptodata/1/pubpaa/USIOB_PUBCOMB.pop:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-164-649-50
US-10-239-423-64
US-10-7439-842-8
US-10-741-601-285
US-10-741-601-286
US-10-791-166-4
US-10-791-166-4
US-10-700-313-8
US-10-486-471-4
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                              OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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Perfect score:
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                                                                                                                                                                                                                                                         Run on:
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No.
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Sequence 20, Appl Sequence 20, Appl Sequence 473, Appl Sequence 7, Appl Sequence 3, Appl Sequence 3, Appl Sequence 14, Appl Sequence 2, Appl Sequence 2, Appl Sequence 2, Appl Sequence 2, Appl Sequence 3, Appl Sequence 3, Appl Sequence 9, Appli	ૢઌઌઌઌ ૣૡૡૡૡ
US-10-846-185-8 US-09-131-827A-20 US-09-826-509-473 US-10-925-095-473 US-09-938-719-7 US-09-938-719-7 US-09-938-719-7 US-10-661-798-7 US-10-661-798-7 US-10-661-798-7 US-10-661-798-7 US-10-164-649-51 US-10-164-649-51 US-10-164-649-51 US-10-16-792-3 US-10-10-16-3 US-10-10-10-3 US-10-10-39-96-3 US-10-799-736-14 US-10-799-736-14 US-10-799-512-13 US-10-799-512-13 US-10-799-512-14 US-10-791-601-287 US-10-791-166-2 US-10-779-8004-9 US-10-232-686-9 US-10-135-839-9	US-09-725-285-9 US-09-195-662A-9 US-09-339-912A-9 US-09-502-783A-9 US-10-791-905-9
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ALIGNMENTS

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61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
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                                                                                                     APPLICANT: O'Brien, Stephen J.
APPLICANT: O'Brien, Stephen J.
APPLICANT: Smith, Michael
APPLICANT: Carrington, Mary
TITLE OF INVENTION: MISSENSE ALLELE OF THE CCR2 GENE
TITLE OF INVENTION: MISSENSE ALLELE OF THE CCR2 GENE
CURRENT APPLICATION NUMBER: US/09/131,827A
CURRENT APPLICATION NUMBER: 60/055,659
PRIOR FILING DATE: 1998-08-10
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSEQ for Windows Version 4.0
                  Sequence 2, Application US/09131827A Patent No. US20020038469A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                                     GENERAL INFORMATION:
JS-09-131-827A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-131-827A-2
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Gaps

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Sequence 50, Application US/10164649
Publication No. US20030162943A1
GENERAL INFORMATION
GENERAL INFORMATION: No. US20030162943A1e1 Molecules of the G Protein-Coupled
APPLICANT: Graham, Gerard J. et al.
TITLE OF INVENTION: No. US20030162943A1e1 Molecules of the G Protein-Coupled
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: BOSECON
STATE: MASSACHUSELTS
COUNTRY: USA
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100.0%; Score 1900; DB 14; Length 360;
Best Local Similarity 100.0%; Pred. No. 4.5e-150;
Matches 360; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/10/164,649
FILING DATE: 07-Jun-2002
CLASSIFICATION: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/045,583
FILING DATE: 20-WAR-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Mandragouras, Amy E. REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MNI-044
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 50:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (617)227-7400
TELEPRA: (617)742-4214
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
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US-10-239-423-64
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APPLICANT: Brown, Joseph P.
APPLICANT: Burmer, Glenna C.
APPLICANT: Roush, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS FILE REFERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: 0310/225,567A
CURRENT FILING DATE: 2001-12-19
PRIOR PILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
SOFTWARE: Patentin version 3.1
SEQ ID NO 460
LENGTH: 360
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4.5e-150;
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; Pred. No. 4.5e
0; Mismatches
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Best Local Similarity 100.0
Matches 360; Conservative
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-10-225-567A-460
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US-10-164-649-50
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Best Local Similarity 100.
Matches 360; Conservative
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LENGTH: 360
TYPE: PRT
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Best Local {
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                                         GENERAL INFORMATION:

APPLICANT: FORSSWANN, Wolf-Georg; FORSSWANN, Ulf; ADERWANN, Knut;

APPLICANT: FORSSWANN, Wolf-Georg; FORSSWANN, Ulf; ADERWANN, Knut;

APPLICANT: HITLAND, Aleksandra; SPODSBERG, Nikolaj

TITLE OF INVENTION: Cell Surface Proteome of Tumor and Inflammation Cells and

TITLE OF INVENTION: For Treating Tumor Diseases and Inflammatory Diseases,

TITLE OF INVENTION: Receptor Analysis and Chemokine Receptor/Ligand Interaction

TITLE OF INVENTION: Receptor Analysis and Chemokine Receptor/Ligand Interaction

TITLE OF INVENTION: Preferably with the Aid of Specific Chemokine

TITLE OF INVENTION: Receptor Analysis and Chemokine Receptor/Ligand Interaction

FILE REPREMENCE: 020217us

CURRENT APPLICATION NUMBER: US/10/239,423

CURRENT PELICATION NUMBER: DISO0-03-31

NUMBER OF SEQ ID NOS: 84

SEQ ID NOS: 84

LENGTH: 360
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Publication No. US20030195348A1
GENERAL INFORMATION:
APPLICANT: Condadiere et al.,
TITLE OF INVENTION: CC CHEMOKINE RECEPTOR 5 DNA, NEW ANIMAL MODELS
TITLE OF INVENTION: AND THERAPEUTIC AGENTS FOR HIV INFECTION
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
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Application US/10239423
No. US20030186889A1
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MEDIUM TYPE: Floppy disk
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STATE: CA
COUNTRY: USA
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Sequence 285, Application US/10741601
GENERAL INFORMATION:
TOTAL OF INVENTION: GENERAL POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1500
CURRENT APPLICATION NUMBER: US/10/741,601
CURRENT APPLICATION NOWER: US/10/741,601
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 26415
SOFTWARE: FASESEQ for Windows Version 4.0
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/439,845
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION NUMBER: 08/864,458
FILING DATE: May 28, 1997
APPLICATION NUMBER: Provisional 60/018,508
FILING DATE: May 28, 1996
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 h 100.0%; Score 1900; DB 14; Similarity 100.0%; Pred. No. 4.5e-150; 60; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08830/030001
                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION TELEPHONE: 619/678-5070
TELEPAX: 619/678-509
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INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
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241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
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ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
STREET: 5 Palo Alto Square
                                                                                                                                                                                                                                                                                                                               APPLICANI: CHEAC, --- Shaun
Coughlin, Shaun
TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
PROTEIN RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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100.0%; Score 1900; DB 16;
Best Local Similarity 100.0%; Pred. No. 4.5e-150;
Matches 360; Conservative 0; Mismatches 0; ]
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REGISTRATION NUMBER: 30,092
REFERENCE/DOCKET NUMBER: UCAL-237/01US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 01-Mar-2004
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/625,573
FILING DATE: 25-Jul-2000
APPLICATION NUMBER: US/08/446,669
FILING DATE: MAY 25, 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/10/791,592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear; ; MOLECULE TYPE: protein; ; SEQUENCE DESCRIPTION: SEQ ID NO: 4: US-10-791-592-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-843-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94306-2155
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                       Sequence 4, Application US/10791592
Publication No. US20040219644A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                      APPLICANT: Charo, Israel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Palo Alto
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US-10-791-592-4
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                                                                                                                                      Gaps
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: CLOO1500
CURRENT APPLICATION NUMBER: US/10/741,601
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 26415
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 286
LENGTH: 360
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                                                                          Length 360;
                                                                                                                                 Indels
                                                                             0; DB 16;
4.5e-150;
                                                                          i; Score 1900; Li; Pred. No. 4.5e0; Mismatches
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Publication No. US20040166519A1
GENERAL INFORMATION:
                                                                          Query Match
Best Local Similarity 100.0%;
Matches 360; Conservative 0
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ORGANISM: Homo sapiens
ORGANISM: Homo sapiens
        ; OKGANISM: DOM: US-10-741-601-285
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                                                                             181 CQKEDSVYVCGPYFPRGWNNPHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240
                                                                                                                                                     241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
                                                                                                                                                                                                                                                       301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL 360
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Publication No. US20040259785A1
GENERAL INFORMATION:
APPLICANT: Combadiere et al.,
TITLE OF INVENTION: CC CHEMOKINE RECEPTOR 5 DNA, NEW ANIMAL MODELS
NUMBER OF SEQUENCES: 9
CORRESPONDEMENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
                                                                                                                                                                                     241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI
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                                                  181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR
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100.0%; Score 1900; DB 16; Length 360;
Best Local Similarity 100.0%; Pred. No. 4.5e-150;
Matches 360; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/864,458 -
FILING DATE: 28-MAY-1997
APPLICATION NUMBER: Provisional 60/018,508
FILING DATE: May 28, 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 08830/030001
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APPLICATION NUMBER: US/10/700,313
FILING DATE: 31-Oct-2003
CLASSIFICATION: 536
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SEQUENCE DESCRIPTION: SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION
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SEQUENCE CHARACTERISTICS
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COMPUTER READABLE FORM:
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US-10-700-313-8
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181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKRRHR 240
                                                                                                                                                  301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL 360
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                                                  241 AVRVIFTIMIVYFLFWTPYNIVILLNTFOEFFGLSNCESTSOLDOATOVTETLGMTHCCI
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TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
PROTEIN RECEPTORS
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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REGISTRATION NUMBER: 30,092
REFERENCE/DOCKET NUMBER: UCAL-237/01US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/625,573
PILING DATE: 25-Jul-2000
APPLICATION NUMBER: US/08/446,669
FILING DATE: May 25, 1995
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/791,166
FILING DATE: 01-Mar-2004
CLASSIPICATION: <Unknown>
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Pred. No. 4.
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MOLECULE TYPE: protein;
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-791-166-4
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ADDRESSEE: Cooley Godward (
STREET: 5 Palo Alto Square
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Publication No. US20040223968A1
GENERAL INFORMATION:
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TYPE: amino acid
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Best Local Similarity 100.0%;
Matches 360; Conservative 0
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SEQUENCE CHARACTERISTICS
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STATE: California
COUNTRY: USA
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CORRESPONDENCE ADDRESS:
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                        121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
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Publication No. US20050118677A1
GENERAL INFORMATION:
APPLICANT: Combadiere et al.,
TITLE OF INVENTION: CC CHEMOKINE RECEPTOR 5 DNA, NEW ANIMAL MODELS
NUMBER OF SEQUENCES: 9
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Gaps
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; APPLICANT: TOPIGEN PHARMACEUTIQUE INC.
; FILE REFERENCE: 009553-0003; CURRENT APPLICATION NUMBER: US/10/486,471; CURRENT PILING DATE: 2004-02-10; PRIOR APPLICATION NUMBER: U.S. 60/311,088; PRIOR PILING DATE: 2001-08-10; NUMBER OF SEQ ID NOS: 20; SOFTWARE: Patentin version 3.1; SEQ ID NO 4; LENGTH: 360
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ORGANISM: Homo sapiens
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Best Local Similarity
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100.0%; Score 1900; DB 17; Length 360;
Best Local Similarity 100.0%; Pred. No. 4.5e-150;
Matches 360; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                  COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/864,458
FILING DATE: May 28, 1997
APPLICATION NUMBER: Provisional 60/018,508
FILING DATE: May 28, 1996
ATTORNEY/AGENT INFORMATION:
STREET: 4225 Executive Square, Suite 1400 CHTY: La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 08830/030001
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/846,185
FILING DATE: 14 May-2004
CLASSIPICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Haile, Lisa A. REGISTRATION NUMBER: 38,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
US-09-131-827A-20
US-09-131-827A-20
; Sequence 20, Application US/09131827A
; Patent No. US20020038469A1
; GENERAL INPORMATION:
; APPLICANT: Dean, Michael
; APPLICANT: O'Brien, Kiephen J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 619/678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
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240
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Pred. No. 1.4e-149;
0; Mismatches 1;
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APPLICANT: Liaw, Chen W.

APPLICANT: Liaw, Chen W.

APPLICANT: Liaw, Chen W.

TITLE OF INVENTION: Non-Endogenous, Constitutively,
TITLE OF INVENTION: Protein-Coupled Receptors

TILE REFERENCE: AREN-207

CURRENT APPLICATION NUMBER: US/10/925,095

CURRENT FILING DATE: 2004-08-24

PRIOR APPLICATION NUMBER: 05/99/826,509

PRIOR PILING DATE: 2001-04-05

PRIOR APPLICATION NUMBER: 06/195,747

PRIOR APPLICATION NUMBER: 06/195,747

PRIOR APPLICATION NUMBER: 09/170,496

PRIOR PILING DATE: 1998-10-13

NUMBER OF SEQ ID NOS: 589

SOFTWARE: Patentin Version 2.1

SEQ ID NO 473
          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 473, Application US/10925095; Publication No. US20050019840A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 99.7%;
Matches 359; Conservative
          359; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Homo sapiens
US-10-925-095-473
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          Matches
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; Sequence 473. Application US/09826509
; Publication No. US20030204073A1
; GRENEAL INFORMATION:
GAPPLICANT: Lehmann-Bruinsma, Karin
HTLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G
TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G
TITLE OF INVENTION: Protein-Coupled Receptors
FILE REFERENCE: AREN-207
; CURRENT PELLING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR PILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 473
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Pred. No. 5.4e-150;
1; Mismatches 0; Indels
APPLICANT: Smith, Michael
APPLICANT: Carrington, Mary
TITLE OF INVENTION: DELANED PROGRESSION TO AIDS BY A
TITLE OF INVENTION: DELANED PROGRESSION TO AIDS BY A
TITLE OF INVENTION: MISSENSE ALLELE OF THE CCR2 GENE
FILE REPERENCE: 14014.0333
CURRENT APPLICATION NUMBER: US/09/131,827A
CURRENT APPLICATION NUMBER: 60/055,659
PRIOR APPLICATION NUMBER: 60/055,659
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PastSEQ for Windows Version 4.0
IENGTH: 360
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Best Local Similarity 99.7
Matches 359; Conservative
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Search completed: June 9, 2005, 17:06:38 Job time: 101.545 secs